

09/03/98

US594 U.S. PTO

UTILITY PATENT APPLICATION TRANSMITTAL (Large Entity)

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Docket No.
9606Z-IYTotal Pages in this Submission
3**TO THE ASSISTANT COMMISSIONER FOR PATENTS**Box Patent Application
Washington, D.C. 20231

Transmitted herewith for filing under 35 U.S.C. 111(a) and 37 C.F.R. 1.53(b) is a new utility patent application for an invention entitled:

NON-PATHOGENIC STRAINS OF HIV-I

and invented by:

Nicholas J. Deacon, et al.

US540 U.S. PTO

09/146783

If a **CONTINUATION APPLICATION**, check appropriate box and supply the requisite information:☒ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.: 08/477,464

Which is a:

☐ Continuation ☐ Divisional ☒ Continuation-in-part (CIP) of prior application No.: 08/388,353

Which is a:

☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.: _____

Enclosed are:

Application Elements

1. ☒ Filing fee as calculated and transmitted as described below
2. ☒ Specification having 395 pages and including the following:
 - a. ☒ Descriptive Title of the Invention
 - b. ☒ Cross References to Related Applications (if applicable)
 - c. ☐ Statement Regarding Federally-sponsored Research/Development (if applicable)
 - d. ☐ Reference to Microfiche Appendix (if applicable)
 - e. ☒ Background of the Invention
 - f. ☒ Brief Summary of the Invention
 - g. ☒ Brief Description of the Drawings (if drawings filed)
 - h. ☒ Detailed Description
 - i. ☒ Claim(s) as Classified Below
 - j. ☒ Abstract of the Disclosure

UTILITY PATENT APPLICATION TRANSMITTAL
(Large Entity)

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3

Application Elements (Continued)

3. ☒ Drawing(s) *(when necessary as prescribed by 35 USC 113)*
- a. ☒ Formal Number of Sheets 101
- b. ☐ Informal Number of Sheets _____
4. ☒ Oath or Declaration
- a. ☐ Newly executed *(original or copy)* ☐ Unexecuted
- b. ☒ Copy from a prior application (37 CFR 1.63(d)) *(for continuation/divisional application only)*
- c. ☐ With Power of Attorney ☐ Without Power of Attorney
- d. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application,
see 37 C.F.R. 1.63(d)(2) and 1.33(b).
5. ☒ Incorporation By Reference *(usable if Box 4b is checked)*
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under
Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby
incorporated by reference therein.
6. ☐ Computer Program in Microfiche *(Appendix)*
7. ☒ Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all must be included)*
- a. ☒ Paper Copy
- b. ☐ Computer Readable Copy *(identical to computer copy)*
- c. ☒ Statement Verifying Identical Paper and Computer Readable Copy

Accompanying Application Parts

8. ☐ Assignment Papers *(cover sheet & document(s))*
9. ☐ 37 CFR 3.73(B) Statement *(when there is an assignee)*
10. ☐ English Translation Document *(if applicable)*
11. ☐ Information Disclosure Statement/PTO-1449 ☐ Copies of IDS Citations
12. ☒ Preliminary Amendment
13. ☒ Acknowledgment postcard
14. ☒ Certificate of Mailing
- ☐ First Class ☒ Express Mail *(Specify Label No.):* EM469617181US

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Accompanying Application Parts (Continued)

15. ☐ Certified Copy of Priority Document(s) (if foreign priority is claimed)

16. ☒ Additional Enclosures (please identify below):

Request to Use Computer Readable Form of Sequence Listing from Another Application under 37 C.F.R. 1.821(e)

Fee Calculation and Transmittal

CLAIMS AS FILED

For	#Filed	#Allowed	#Extra	Rate	Fee
Total Claims	138	- 20 =	118	x \$22.00	\$2,596.00
Indep. Claims	22	- 3 =	19	x \$82.00	\$1,558.00
Multiple Dependent Claims (check if applicable) <input checked="" type="checkbox"/>					\$270.00
BASIC FEE					\$790.00
OTHER FEE (specify purpose)					\$0.00
TOTAL FILING FEE					\$5,214.00

- ☒ A check in the amount of \$5,214.00 to cover the filing fee is enclosed.
- ☒ The Commissioner is hereby authorized to charge and credit Deposit Account No. 19-1013SSMP as described below. A duplicate copy of this sheet is enclosed.
- ☐ Charge the amount of _____ as filing fee.
- ☒ Credit any overpayment.
- ☒ Charge any additional filing fees required under 37 C.F.R. 1.16 and 1.17.
- ☐ Charge the issue fee set in 37 C.F.R. 1.18 at the mailing of the Notice of Allowance, pursuant to 37 C.F.R. 1.311(b).

Signature

Leopold Presser, Reg. No. 19,827
Scully, Scott, Murphy & Presser
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343

Dated: September 3, 1998

CC:

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Nicholas J. Deacon, **Examiner:** J. Parkin
et al.

Serial No.: Unassigned

Art Unit: 1648

Filed: herewith

Docket: 9606Z-IY

For: NON-PATHOGENIC STRAINS
OF HIV-1

Dated: September 3, 1998

Assistant Commissioner for Patents
Washington, DC 20231

PRELIMINARY AMENDMENT

Sir:

Prior to examination, please amend the above-identified patent application as follows:

IN THE SPECIFICATION

Please replace the paragraph under "**CROSS REFERENCE TO RELATED APPLICATION**" to read as follows:

--The present application is a continuation application of Serial Number 08/477,464 filed on June 7, 1995 which is a continuation-in-part of application Serial No. 08/388,353 filed on February 14, 1995.--

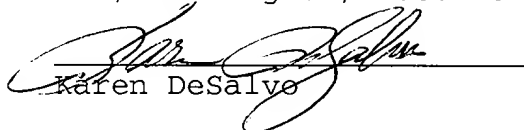
Please renumber pages 212 to 284 as pages 323-395.

CERTIFICATE OF MAILING BY "EXPRESS MAIL"

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Date of Deposit: September 3, 1998

I hereby certify that this correspondence is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. §1.10 on the date indicated above and is addressed to the Assistant Commissioner of Patents and Trademarks, Washington, D.C. 20231.

Dated: September 3, 1998


Karen DeSalvo

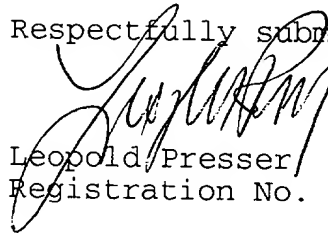
REMARKS

The present application is a continuation application under 37 C.F.R. 1.53(b).

Applicants have amended the specification to include cross-reference to the relevant chain of applications and have renumbered certain pages of the specification.

It is respectfully requested that this Preliminary Amendment be entered in this application prior to examination. Early and favorable allowance is requested.

Respectfully submitted,


Leopold Presser
Registration No. 19,827

SCULLY, SCOTT, MURPHY & PRESSER
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343

ARP:ae

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NON-PATHOGENIC STRAINS OF HIV-1

CROSS REFERENCE TO RELATED APPLICATION

- 5 This application is a continuation-in-part application of US Serial No. 388,353 filed on 14 February, 1995.

FIELD OF THE INVENTION

- 10 The present invention relates to non-pathogenic strains of HIV-1 and to components, parts, fragments and derivatives thereof and to genetic sequences derived therefrom and their use in the development of diagnostic and therapeutic compositions for the treatment and prophylaxis of AIDS and AIDS-related disorders. The present invention also relates to a method for attenuating pathogenic strains of HIV-1 by mutagenizing particular regions of the HIV-1 genome. A particularly useful aspect of the present invention is
- 15 a method for determining the likelihood or otherwise of an individual who is seropositive for HIV-1 developing AIDS or AIDS-related symptoms. Another aspect of the present invention is directed to strains of HIV-1 capable of synthesizing a modified Nef protein or having a wild-type Nef protein modified after synthesis thereby rendering those strains of HIV-1 substantially non-pathogenic.

20

BACKGROUND OF THE INVENTION

- Bibliographic details of the publications referred to in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide and amino acid sequences referred to in the specification are defined
- 25 following the bibliography.

- Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but
- 30 not the exclusion of any other element or integer or group of elements or integers.

Genomic nucleotide sequences of HIV-1 strains referred to herein are represented by their corresponding DNA sequence.

- 5 Exemplary viral isolates referred to herein as "C18" and "C98" were deposited at the PHLS Centre for Applied Microbiology and Research, European Collection of Animal Cell Cultures (ECACC), Division of Biologies, Porton Down, Salisbury, Wiltshire SP4 OJG. C18 was deposited on 17 October, 1994 under Provisional Accession Number V94101706 and C98 was deposited on 31 October, 1994 under Provisional Accession
10 Number V941031169. Viral isolate "C54" was deposited at ECACC on 10 March, 1995 under Provisional Accession Number V95031022.

A summary of particular deletion mutants of HIV-1 of the present invention referred to herein is given in Figure 11.

15

- Acquired Immune Deficiency Syndrome (AIDS) and AIDS related disorders are the clinical result of infection by Human Immunodeficiency Virus type I (HIV-1) (Barre-Sinoussi *et al*, 1983). Infection by HIV-1 is generally characterised by progressive immune system damage (Teeuwssen *et al*, 1990; Clerici *et al*, 1989) leading to
20 opportunistic infections, malignancies or wasting syndrome that constitute clinically-defined AIDS (Busch *et al*, 1991; Klaslow *et al*, 1990).

- The high mortality rate of individuals infected with HIV-1 together with the social and economic consequences of the continuing HIV-1 epidemic has created an urgent need
25 for a safe and effective treatment and/or prophylaxis against the devastating effects of AIDS. However, despite over a decade of high level scientific research into the pathogenesis of HIV-1 and the clinical manifestations of the disease, together with a detailed molecular analysis of the virus, there has been little success in the development of an effective vaccine. To date, the most effective therapy is treatment with zidovudine
30 (AZT) which delays the onset of full blown AIDS and alleviates to some extent the symptoms of HIV-1 infection. However, AZT is not an innocuous compound and AZT, metabolic products thereof or impurities therein can cause a number of side effects

which limit long term treatment with the drug. Furthermore, AZT resistant isolates have been reported during treatment. Clearly, therefore, a need exists to develop alternative strategies in preventing and treating HIV-1 infection.

- 5 The initial phases of HIV-1 infection are summarised by Levy (1993) as involving attachment, fusion and nucleocapsid entry. These phases have been the traditional foci in research into development of antiviral strategies. The molecular events at the virus genomic level have also been the subject of intense scientific research with an aim being the development of a live attenuated vaccine as a possible approach for the treatment or
- 10 prophylaxis of HIV-1 infection.

There is a high variable rate of progression from initial HIV-1 infection to AIDS which reflects a rapidly changing pathogen and variable immune response of the host to infection (Sheppard *et al*, 1993). With regards to the latter, HIV-1 can be considered

15 as a heterogenous group of viruses differing at the genetic level with concomitant variable pathogenicity. For example, HIV-1 strains can differ in their capacity to kill cells. Furthermore, it appears that HIV-1 strains evolve in a host after infection and that the evolution varies depending on the tissues infected by the virus. The major sites in the genome apparently responsible for biological and pathological variation are the

20 highly variable envelope region (Cheng-Mayer *et al*, 1991; Shioda *et al*, 1992; Hwang, *et al* 1991; Sullivan *et al*, 1993; Groenink *et al*, 1993) and the viral regulatory regions such as *tat* (Leguern *et al*, 1993). The genetic complexity of the HIV-1 group of viruses together with their variable pathogenicity, are major difficulties in the development of live vaccines, genetic vaccines or component vaccines.

- 25 Notwithstanding the highly pathogenic nature of HIV-1, there are some reports of long term survival of subjects infected with the virus (Learmont *et al*, 1992; Levy, 1993; Sheppard *et al*, 1993; Lifson *et al* 1991). It is not always clear, however, whether a benign course following HIV-1 infection is due to host factors, viral factors or other
- 30 unknown factors. There are reports that most infected people have at least laboratory evidence of progressive immune system damage in the form of CD4+ cell loss (Lang *et al*, 1989) and defective immune responses (Clerici *et al*, 1989).

Although simian monkeys have been used as an *in vivo* model for HIV and Simian Immunodeficiency Virus (SIV) infection, a major handicap in AIDS research has been the absence of suitable *in vivo* models to study the pathogenesis of the disease and, in particular, to study the viruses involved in benign infection. The need for a suitable *in vivo* model is heightened by the fact that results obtained *in vitro* cannot necessarily be extrapolated to what occurs *in vivo*. This was clearly observed by Mosier *et al* (1993) where conflicting results were obtained in animals compared to cell cultures.

- Despite the absence of suitable *in vivo* models, considerable scientific research has been directed to attenuating HIV-1 strains by mutagenesis of the virus genome. Deletions in the *nef* gene have been implicated in attenuated strains of SIV and their use in providing protective effects in monkeys (Daniel *et al*, 1992). However, there are conflicting reports on the possible negative influence the *nef* gene product has on the rate or extent of virus replication (Terwilliger *et al*, 1986; Luciw *et al*, 1987; Niederman *et al*, 1989; Kim *et al*, 1989; Hammes *et al*, 1989). In fact, Kim *et al* (1989) found that *nef* did not affect HIV-1 replication or HIV-1 long terminal repeat (LTR)-driven CAT expression. Kestler III *et al* (1991) found that the *nef* gene is required for full pathogenic potential in SIV. However, such is the complexity of the HIV-1 group of viruses and the variability of immune responses between individuals let alone different species, that it is far from clear whether *nef* deleted strains of HIV-1 would behave similarly to *nef* deleted strains of SIV-I. There is a need, therefore, in order to investigate the possibility of *nef* deleted HIV-1 strain as a vaccine candidate, to identify individuals infected with such modified viruses.
- Learmont *et al* (1992) reported that a cohort of five persons infected with blood products from a single HIV-1 infected donor have remained asymptomatic from up to about 10-14 years after infection. Subsequently, a sixth person has been identified as being part of the cohort. Both the donor and recipients were HIV-1 seropositive but with no indications of clinical symptoms of HIV-1 related disease and CD4+ cell number and β_2 -microglobulin levels have remained in the normal range. The identification of this cohort of benignly infected individuals provides a unique *in vivo* model in which the pathogenesis of HIV-1 infection can be studied at the clinical and molecular biological

levels.

However, it has not always been possible using conventional isolation procedures to routinely and reproducibly isolate viral strains from the above mentioned donor or recipients which has frustrated efforts to investigate the cause of the asymptomatic individuals. In accordance with the present invention, methods have now been established to isolate viruses from the above individuals. It has been determined, in accordance with the present invention, that individuals of the cohort are infected by non-pathogenic strains of HIV-1. Furthermore, the non-pathogenic strains of HIV-1 carry one or more nucleotide mutations. The non-pathogenic strains of the present invention enable the generation of a range of therapeutic, diagnostic and targeting agents against HIV-1 infection. The present invention also enables the attenuation of previously pathogenic strains of HIV-1. Additionally, an investigation of the immunological profiles of cohort individuals has revealed that a non-pathogenic strain of HIV-1 is indicated by a particular deletion in the coding region of a protein resulting in an altered immunological profile for the expressed protein. An example of an altered immunological profile results from a deletion of certain amino acids in the Nef protein.

SUMMARY OF THE INVENTION

One aspect of the invention is directed to an isolated HIV-1 strain or a component, part, fragment or derivative thereof which is substantially non-pathogenic.

Another aspect of the invention is directed to an isolated strain of HIV-1 or a biological source thereof, said HIV-1 having the following characteristics:

- (i) is substantially non-pathogenic in human subjects; and
 - (ii) carries a modified *nef* gene which encodes a *nef* gene product substantially immunologically non-interactive with antibodies to amino acids 162 to 177 of Nef in wild-type HIV-1.
- Yet another aspect of the invention is directed to an isolated non-pathogenic strain of HIV-1 comprising a genome which is substantially incapable of hybridizing under medium stringent conditions to a nucleic acid molecule comprising a sequence of

nucleotides which encodes all or part of amino acids 162 to 177 of wild-type HIV-1 Nef.

Still another aspect of the invention provides a non-pathogenic HIV-1 isolate which:

- 5 (i) induces an immune response in a human or primate subject;
 (ii) does not substantially produce a proliferative response or cytokine
 production to a mitogen, alloantigen and/or recall antigen relative to a
 healthy, non-infected subject; and
 (iii) is substantially incapable of inducing an antibody response to amino acids
 10 162 to 177 of wild-type HIV-1 Nef protein.

Still yet another aspect of the invention contemplates a viral isolate which:

- 15 (i) is interactive to antibodies to a glycoprotein from HIV-1 selected from gp41-45, gp120 and gp160;
- (ii) is substantially non-pathogenic in human subjects; and
- (iii) carries a deletion mutation of at least ten nucleotides in a region corresponding to all or part of amino acids 162 to 177 encoded by the *nef* gene of a pathogenic strain of HIV-1.

20 Another aspect of the invention provides an isolated strain of HIV-1 which is reactive to antibodies to a glycoprotein of HIV-1, is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env* and which is incapable of directing synthesis of a *nef* gene product or a full length *nef* gene product.

25 A further aspect of the invention contemplates a method for inhibiting or reducing productive infection of an individual by a pathogenic strain of HIV-1, said method comprising administering to a subject a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate target cells carrying DNA derived from said non-pathogenic HIV-1.

In yet another aspect of the invention there is contemplated a method for vaccinating an individual against the development of AIDS or AIDS related diseases, said method comprising administering to said individual a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate target cells carrying DNA derived from said non-pathogenic HIV-1.

In still yet another aspect of the invention there is provided a method for obtaining a preparation of non-pathogenic HIV-1 from a biological sample, said method comprising co-culturing PBMCs from said biological sample from an individual putatively infected with said non-pathogenic HIV-1 with HIV-1 seronegative donor PBMCs depleted for CD8+ cells, harvesting the PBMCs and supernatant fluid every from about 5 to about 10 days and adding fresh medium with CD8+ depleted PBMCs with said fresh medium and isolating said virus from the supernatant fluid.

Another aspect of the invention contemplates a method for obtaining a preparation of non-pathogenic HIV-1 from a biological sample, said method comprising co-culturing monocytes from said biological sample from an individual putatively infected with said non-pathogenic HIV-1 with HIV-1 seronegative donor PBMCs depleted for CD8+ cells, harvesting the monocytes and PBMCs and supernatant fluid every from about 5 to about 10 days and adding fresh medium with CD8+ depleted PBMCs with said fresh medium and isolating said virus from the supernatant fluid.

In yet a further aspect of the invention there is contemplated a method for identifying or screening for compounds capable of reducing or otherwise interfering with HIV-1 replication, said method comprising contacting a compound to be tested with a cell or cell extract containing or capable of containing a *nef* gene product fused to a reporter molecule capable of giving an identifiable signal and screening for a compound which inhibits said signal.

In still yet a further aspect of the invention there is provided a viral isolate which:

- (i) is genetically or immunologically related to a pathogenic strain of HIV-1;
 - (ii) is substantially non-pathogenic in human subjects;
 - 5 (iii) comprises a first nucleotide sequence constituting its genome which is capable of hybridising under medium stringency conditions to SEQ ID NO: 1 or a complementary form thereof; and
 - (iv) comprises a second nucleotide sequence within said first nucleotide
10 sequence and which second nucleotide sequence directs expression of a mRNA molecule capable of inhibiting, reducing or otherwise down-regulating translation of a protein or polypeptide encoded by a pathogenic strain of HIV-1 or inhibit, reduce or otherwise down regulate operation of a non-protein encoding a region of a pathogenic strain of HIV-1.
- 15 Still yet another aspect of the invention is directed to a method for determining the pathogenicity of an HIV-1 strain after said HIV-1 strain infects cells of an individual, said method comprising determining the presence of a deletion mutation in the genome of said HIV-1 wherein said deletion mutation results in said genome being unable to synthesize a polypeptide or protein from a pathogenic strain of HIV-1 or directing the
20 synthesis of a truncated form of said polypeptide or protein wherein the presence of a such a mutation is indicative of the presence of a non-pathogenic strain of HIV-1.

A further aspect of the invention contemplates a method for determining the pathogenicity of a strain of HIV-1 after said HIV-1 strain infects cells of an individual,
25 said method comprising contacting a biological sample from said individual with a peptide corresponding to a deleted or truncated region of an HIV-1-derived protein and screening for the absence of antibody binding to said peptide, wherein the absence of antibody binding is indicative of a deletion or truncation in that protein and further indicative of the non-pathogenicity of said strain of HIV-1.

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BRIEF DESCRIPTION OF THE FIGURES

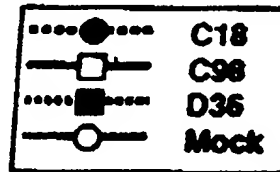
- Figure 1 is a representation showing the alignment of the nucleotide sequences from donor D36 peripheral blood mononuclear cell (PBMC) [D36P] and non-pathogenic HIV-1 from recipient C18 HIV_{SV} [C18S], C18 HIV_{MBC} [C18M] and C98 HIV [C98H] and C54 PBMC [C54P] with the equivalent region of HIV-1_{NL43}. Sequences labelled PBMC are from patient PBMC, those labelled HIV are from virus isolated from patient PBMC and grown in culture. Numbering for HIV-1_{NL43} is as per Myer *et al* (1992; 1994) where nucleotide 1 is the first nucleotide of the complete proviral DNA sequence.
- D36P, C18S, C18M, C98H and C54P are numbered from the start of the region sequenced. Identity with NL43 sequence is shown by (*). Deleted nucleotides are shown by (-). Spaces introduced to maximise alignment are shown by (.). Features in HIV-1_{NL43} are marked by overlining the sequence, features in D36 and C18 are marked by underlining the sequence.
- Figure 2 shows the alignment of encoded amino acid sequences of (a) *tat* exon 3 and (b) *rev* exon 3 from HIV-1_{NL43}, D36 PBMC, C18 HIV_{SV} and C98 HIV. In-phase termination codons (*) and NL43 encoded amino acid numbers are shown.
- Figure 3 is a representation showing the alignment of C-terminal envelope glycoprotein gp41 amino acid sequences encoded by D36 PMBC, C18 HIV_{SV}, C18 HIV_{MBC} and C98 HIV. Numbering is that of the amino acid sequence of the mature envelope glycoprotein of HIV-1_{NL43}. Termination is shown by (#).
- Figure 4 is a representation showing alignment of amino acid sequences encoded by the *nef* genes of HIV-1_{NL43}, D36 PBMC, C18 HIV_{SV}, C18 HIV_{MBC} and C98 HIV. In phase termination codons are shown by (#). Identical amino acids are shown by (*). Residues underlined are those immediately before a deletion.
- Figure 5 shows a duplication of NFκB and Sp1 sequences in D36 PBMC, C18 HIV_{SV}, C18 HIV_{MBC} and C98 HIV demonstrated by alignment of their low homology region sequences with the NFκB-Sp1 region of HIV-1_{NL43}. Nucleotide numbering according

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- 11 -

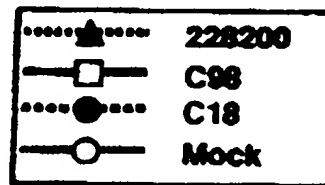
to Figure 1. Identity with NL43 sequence shown by (*) and NFkB and Sp1 sites in NL43 overlined. Position of *nef*/LTR region sequence deletion shown by (Δ).

Figure 6 is a graphical representation showing replication of C18 and C98 viral isolates and D36 PBMCs from asymptomatic patients in PHA-stimulated PBMCs.



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Figure 7 is a graphical representation showing replication of viral isolates from asymptomatic patients in non-PHA stimulated PBMCs.



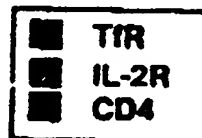
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228200 is an Australian isolate of HIV-1 described by Kiernan, R. *et al* (1990). Its characteristics include being T cell trophic, with fast kinetics, high producer of HIV-1 and/or SI phenotype.

20

Figure 8 is a graphical representation of cell surface receptor expression for syncytia-inducing (SI)/ non-syncytia-inducing (NSI)/asymptomatic patient isolates.

25



228200 is defined in the legend to Figure 7. 243925 is a viral isolate of HIV-1 which is monocyte/macrophage trophic and exhibits NSI phenotype (Dr Karen Coats-Fryer, PhD thesis entitled "Viral determinants of HIV-1 syncytium formation", the University of Melbourne, Parkville, Victoria, Australia).

30

Figure 9 is a representation of the nucleotide sequence of C18 HIV-1_{MBC} (SEQ ID NO: 800).

Figure 10(a) - (g) are graphical representations showing clinical immunology of cohort;
 5 (a) CD3; (b)(i) CD4 (ii) CD4%; (c)(i) CD8; (ii) CD8%; (d) lymphocyte count; (e)
 CD4/CD8 ratio; (f) β -2-microglobulin; and (g) Kaplan-Meier estimates of time to
 disease progression (Cox & Oakes, 1989).

Figure 11 is a schematic representation of the deletion mutants of the present invention.

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Figure 12 shows reactivity of sera from LTP individuals (1a); HIV-1-ve individuals
 (1bi, 1bii); individuals with autoimmune disease (A/HIV-1) (1biii); LTNP1 (1c) and
 LTNP2 (1d) with full length Nef 27 derived from HIV-1_{NL43} (referred to herein as "Nef
 27"). The term "LTNP" is an abbreviation for "Long Term Non-Progressor". NTNP1
 15 and LTNP2 are defined in Example 16.

Wells of 96-well polystyrene microtitre plates coated with purified Nef 27 (100 ng/well)
 were incubated with sera (titrated from 1:100 to 1:10,000) obtained from LTP
 individuals, HIV-1-ve individuals, individuals with autoimmune disease, LTNP1 and
 20 LTNP2. The presence of antibodies in the sera which recognise Nef 27 were detected
 using a biotin-streptavidin HRP system with *o*-phenylenediamine as substrate.
 Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450
 nm.

25 Figure 13a shows reactivity of sera from LTP individuals against Nef-derived peptides.
 Synthetic peptides corresponding to amino acid residues 1 to 19 (i), 20 to 36 (ii), 44 to
 65 (iii); 72 to 83 (iv), 89 to 97 (v); 109 to 114 (vi), 164 to 186 (vii), 187 to 206
 (viii), 121 to 135 (ix) and 162 to 177 (x) of HIV-1_{NL43} Nef 27 were coated onto wells
 of 96-well microtitre plates at a concentration of 500 ng/well. Sera (titrated from 1:300
 30 to 1:100,000) from the LTP individuals were then incubated with the immobilised
 peptides and the presence of antibodies in the sera which recognise the Nef-derived
 peptide were detected using a biotin-streptavidin HRP system with *o*-phenylenediamine

as substrate. Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450 nm.

- Figure 13b(i) shows reactivity of sera from HIV-1-ve individuals against Nef-derived peptides. Synthetic peptides corresponding to amino acid residues 1 to 19(i), 20 to 36 (ii), 44 to 65 (iii), 72 to 83 (iv), 89 to 97 (v), 109 to 114 (vi), 164 to 186 (vii), 187 to 206 (viii), 121 to 135 (ix) and 162 to 177 (x) of HIV-1_{NL43} Nef were coated onto wells of 96-well microtitre plates at a concentration of 500 ng/well. Sera (titrated from 1:300 to 1:100,000) from A/HIV-1-ve individuals with autoimmune disease was then incubated with the immobilised peptides and the presence of antibodies in the sera which recognise the Nef-derived peptides were detected using a biotin-streptavidin HRP system with o-phenylenediamine as substrate. Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450 nm.
- Figure 13b(ii) shows reactivity of sera from autoimmune A/HIV-1-ve individuals against Nef-derived peptides. Synthetic peptides corresponding to amino acid residues 1 to 19 (i), 20 to 36 (ii), 44 to 65 (iii), 72 to 83 (iv), 89 to 97 (v), 109 to 114 (vi), 164 to 186 (vii), 187 to 206 (viii), 121 to 135 (ix) and 162 to 177 (x) of HIV-1_{NL43} Nef were coated onto wells of 96-well microtitre plates at a concentration of 500 ng/well. Sera (titrated from 1:300 to 1:100,000) from A/HIV-1-ve individuals with autoimmune disease was then incubated with the immobilised peptides and the presence of antibodies in the sera which recognise the Nef-derived peptides were detected using a biotin-streptavidin HRP system with o-phenylenediamine as substrate. Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450 nm.
- Figure 13c shows reactivity of sera from LTNP1 individuals against Nef-derived peptides. Synthetic peptides corresponding to amino acid residues 1 to 19 (i), 20 to 36 (ii), 44 to 65 (iii), 72 to 83 (iv), 89 to 97 (v), 109 to 114 (vi), 164 to 186 (vii), 187 to 206 (viii), 121 to 135 (ix) and 162 to 177 (x) of HIV-1_{NL43} Nef were coated onto wells of 96-well microtitre plates at a concentration of 500 ng/well. Sera (titrated from 1:300 to 1:100,000) from the LTNP1 individuals were then incubated with the immobilised peptides and the presence of antibodies in the sera which recognise the Nef-derived

- 14 -

peptides were detected using a biotin-streptavidin HRP system with *o*-phenylenediamine as substrate. Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450 nm.

- 5 Figure 13d shows reactivity of sera from LTNP2 individuals against Nef-derived peptides. Synthetic peptides corresponding to amino acid residues 1 to 19 (i), 20 to 36 (ii), 44 to 65 (iii), 72 to 83 (iv), 89 to 97 (v), 109 to 114 (vi), 164 to 186 (vii), 187 to 206 (viii), 121 to 135 (ix) and 162 to 177 (x) of HIV-1_{NL43} Nef were coated onto wells of 96-well microtitre plates at a concentration of 500 ng/well. Sera (titrated from 1:300
- 10 to 1:100,000) from the LTNP2 individuals were then incubated with the immobilised peptides and the presence of antibodies in the sera which recognise the Nef-derived peptides were detected using a biotin-streptavidin HRP system with *o*-phenylenediamine as substrate. Absorbance was measured using a Titertek plate reader at wavelengths of 630 and 450 nm.

15

A summary of the SEQ ID Nos. used in the subject specification is shown below:

5	SEQ ID NO:	DESCRIPTION
	1	Nucleotide sequence of HIV-1 _{NL43} genome
	2-613	Decanucleotides of <i>nef</i> gene from HIV-1 _{NL43}
10	614	Partial nucleotide sequence of D36 HIV-1 isolate
	615	Partial nucleotide sequence of C18 HIV-1 _{MBC} isolate
	616-625	PCR primers shown in Table 1
	626-633	Sequence primers shown in Table 2
	634	Amino acid residues 15-27 of HIV-1 _{NL43} <i>nef</i> protein
15	635	HIV-1 _{NL43} <i>tat</i> exons (Figure 2)
	636	HIV-1 D36 <i>tat</i> exons (Figure 2)
	637	HIV-1 C18 <i>tat</i> exons (Figure 2)
	638	HIV-1 _{NL43} <i>rev</i> exons (Figure 2)
	639	HIV-1 D36 <i>rev</i> exons (Figure 2)
20	640	HIV-1 C18 <i>rev</i> exons (Figure 2)
	641	HIV-1 _{NL43} C-terminal of gp41 (Figure 3)
	642	HIV-1 D36 C-terminal of gp41 (Figure 3)
	643	HIV-1 C18 C-terminal of gp41 (Figure 3)
	644	HIV-1 _{NL43} <i>nef</i> gene (Figure 4)
25	645	HIV-1 D36 <i>nef</i> gene (Figure 4)
	646	HIV-1 C18 <i>nef</i> gene (Figure 4)
	647	HIV-1 _{NL43} NFkB/SP1 sequence (Figure 5)
	648	HIV-1 D36 NFkB/SP1 sequence (Figure 5)
	649	HIV-1 C18 NFkB/SP1 sequence (Figure 5)
30	650	Nucleotide sequence of <i>nef</i> gene from HIV-1 _{NL43}
	651	Nucleotide sequence of <i>env</i> and <i>nef</i> regions of HIV-1 _{NL43}
	652-799	Decanucleotides of LTR region from HIV-1 _{NL43}
	800	Nucleotide sequence of C18 HIV-1 _{MBC}
	801	Amino acids 162 to 177 of wild-type HIV-1 _{NL43} Nef
35	802	Nucleotide sequence encoding amino acids 162 to 177 of wild-type HIV-1 _{NL43} Nef
	803-841	Decanucleotide deletion of Nef gene covering amino acids 162 to 177

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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

One aspect of the present invention contemplates a non-pathogenic isolate of HIV-1 or a component, part, fragment or derivative thereof.

5

In a related embodiment, there is provided a novel isolate of HIV-1 or a component, part, fragment or derivative thereof wherein said HIV-1 isolate is capable of stimulating in a human or primate subject an immune response such as a humoral immune response to at least one HIV-1 glycoprotein such as but not limited to gp41-45, gp120 and/or gp160 while not substantially reducing in said human or primate subject proliferative responses and cytokine production to a mitogen, alloantigen and/or recall antigen compared to a healthy, non-infected human or primate subject. Preferably, the cytokine is IL-2. Preferably, the mitogen is ConA or PHA and the recall antigen is influenza or tetanus toxoid. Preferably, the HIV-1 isolate is non-pathogenic.

15

More particularly, the present invention relates to an isolated HIV-1 strain which:

- (i) is substantially non-pathogenic in human subjects; and
- (ii) carries one or more mutations in its genome resulting in the inability to direct synthesis of at least one pathogenic HIV-1-derived polypeptide or protein.

20

Even more particularly, the present invention provides an isolated HIV-1 strain which:

- (i) is substantially non-pathogenic in human subjects; and
- (ii) carries a mutation in the *nef* gene and/or a long terminal repeat (LTR) region or in a functionally equivalent location in the HIV-1 genome.

25

Still even more particularly, the present invention is directed to an isolated virus which:

- (i) has a genome which is capable of hybridising under medium stringency conditions to complementary nucleic acid from a pathogenic strain of HIV-1;
- (ii) is substantially non-pathogenic in human subjects;
- 30 (iii) carries one or more deletion mutations in a region of its genome corresponding to a *nef* gene in said pathogenic strain of HIV-1; and
- (iv) optionally carries a mutation in one or both LTR regions.

- 17 -

In a related embodiment, there is provided an isolated virus which:

- (i) has a genome which is capable of hybridising under medium stringency conditions to complementary nucleic acid from a pathogenic strain of HIV-1;
- (ii) is substantially non-pathogenic in human subjects;
- 5 (iii) carries one or more deletion mutations in an LTR region of its genome; and
- (iv) optionally carries a mutation in a region corresponding to a *nef* gene in said pathogenic strain of HIV-1.

In a further related embodiment, there is provided an isolated virus which:

- 10 (i) has a genome which is capable of hybridising under medium stringency conditions to complementary nucleic acid from a pathogenic strain of HIV-1;
- (ii) is substantially non-pathogenic in human subjects; and
- (iii) carries one or more deletion mutations in a region of its genome corresponding to a region which contains *nef* coding sequences and LTR nucleotide sequences.

15

Another aspect of the present invention is directed to an isolated strain of HIV-1 or a biological source thereof, wherein said HIV-1 has the following characteristics:

- (i) is substantially non-pathogenic in human subjects; and
- (ii) carries a modified *nef* gene which encodes a *nef* gene product substantially immunologically non-interactive with antibodies to amino acids 162 to 177 of Nef in wild-type HIV-1.

20

Amino acids of 162-177 of wild-type HIV-1_{NL43} strain (Myers *et al.*, 1994) [hereinafter referred to as "HIV-1_{NL43}"] are as follows:

25

Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu [SEQ ID NO:801].

This aspect of the present invention relates in part to amino acid sequence SEQ ID NO:801 from HIV-1_{NL43} or from the functionally equivalent region of other pathogenic strains of HIV-1.

30

A further aspect of the present invention contemplates an isolated strain of HIV-1 or a biological source thereof, wherein said HIV-1 has the following characteristics:

- (i) is substantially non-pathogenic in human subjects; and
- 5 (ii) encodes an Nef protein or portion thereof which is interactive with wild-type HIV-1 Nef antibodies but which is substantially non-interactive with antibodies to amino acids 162 to 177 of wild-type HIV-1 Nef protein.

Still another aspect of the present invention relates to an isolated strain of HIV-1 or a
10 biological source thereof which is substantially non-pathogenic in human subjects and which is substantially incapable of directing synthesis of a Nef protein or portion thereof comprising amino acids 162 to 177 of wild-type HIV-1 Nef protein.

In still yet another aspect of the present invention, there is provided an isolated strain
15 of HIV-1 or a biological source thereof, said HIV-1 being substantially non-pathogenic in humans and comprising a mutation in its genome corresponding to amino acids 162 to 177 of wild-type HIV-1 Nef such that these amino acids are substantially not represented in a Nef protein or derivative thereof produced by said isolated HIV-1 strain, or insufficient of the amino acid sequence is represented to induce an immune response
20 to that region of Nef.

In a related embodiment, the genomic mutation in the non-pathogenic strain of HIV-1 is a mutation in one or more of nucleotides 9271 to 9317 relative to HIV-1_{NL43} or in a functionally equivalent region in another pathogenic strain of HIV-1.

25

In a related embodiment, there is provided a non-pathogenic strain of HIV-1 comprising a genome which is substantially incapable of hybridising under medium stringent conditions a nucleic acid molecule comprising that sequence of nucleotides which encodes all or part of amino acids 162 to 177 of wild-type HIV-1. Preferably, the
30 nucleic acid molecule is a synthetic oligonucleotide.

In a particularly preferred embodiment, the present invention provides non-pathogenic HIV-1 isolate C18 deposited at the ECACC on 17 October, 1994 under Provisional Accession Number V94101706.

5

In a related embodiment, the present invention provides non-pathogenic HIV-1 isolate C98 deposited at the ECACC on 31 October, 1994 under Provisional Accession Number V941031169.

- 10 In another embodiment, the present invention provides non-pathogenic HIV-1 isolate C54 deposited at ECACC on 10 March, 1995 under Provisional Accession No. V95031022.

- 15 Although pathogenicity is a relative term, it is used herein in relation to the capacity of a strain of HIV-1 to induce AIDS or AIDS-related disorders in an individual over time. Accordingly, a "non-pathogenic" strain of HIV-1 is a strain which, at the clinical level, does not lead to the development of AIDS, at least within the median time of 6-10 years following infection with HIV-1. At the laboratory level, a non-pathogenic strain of HIV-1 is considered not to alter CD4+ cell counts or β_2 -microglobulin concentrations.
- 20 In addition, a non-pathogenic strain of HIV-1 may not alter CD8+ and CD3+ cell counts and would not alter lymphocyte counts. CD4+:CD8+ ratios also remain unchanged relative to normal non-infected individuals. Furthermore, generally, a non-pathogenic strain of HIV-1 does not induce p24 antigenaemia. A non-pathogenic HIV-1 of the present invention is generally still infectious but individuals infected with the virus
- 25 remain free of symptoms for at least 6-10 years after infection.

- A laboratory classified non-pathogenic strain of HIV-1 may be determined at any time after infection. The term "non-pathogenic" is not to be considered as a strain that is never pathogenic under any conditions as this might depend on the host individual, the
- 30 level of immune responsiveness in that individual and the extent or otherwise of other, for example, immune comprising disorders. Accordingly, a "non-pathogenic" HIV-1 isolate of the present invention may also be considered a "low virulent" strain of the

- 20 -

virus. A non-pathogenic strain of HIV-1 as contemplated herein may be isolated from an asymptomatic individual or may be derived from a pathogenic strain by mutation. Although the present invention is not to be limited to any particular pathogenic strain of HIV-1, for reference purposes, an example of a pathogenic strain is HIV-1_{NL43} strain
5 as described by Myers *et al* (1992; 1994).

The non-pathogenic nature of the HIV-1 of the present invention is conveniently evidenced by the cohort of seven individuals comprising one donor and six recipients which have remained free of symptoms or signs of HIV-1 infection for greater than the
10 median time of 6-10 years. However, the individuals of the cohort are seropositive for HIV-1 following infection with the virus as determined by Western blot analysis and genetic analysis (e.g. using PCR techniques). A seropositive individual is one showing reactivity to at least one HIV-1 glycoprotein (such as but not limited to gp 41-45, gp120, gp160) and at least three other virus-specific bands.

15

In accordance with the present invention, a non-pathogenic HIV-1 isolate is also a strain of HIV-1 which:

- (i) induces an immune response in a human or primate subject; and
- (ii) does not substantially reduce proliferative responses or cytokine production to a
20 mitogen, alloantigen and/or recall antigen relative to a healthy, non-infected subject.

Preferably, the immune response such as to a glycoprotein, for example gp41-45, gp120 and/or gp160. Preferably, the cytokine monitored is an interleukin, such as IL-2.
25 Preferably, the recall antigen is influenza or tetanus toxoid. A non-pathogenic HIV-1 isolate is also one which:

- (iii) does not substantially alter proliferative responses or cytokine production to allogeneic mononuclear cells.
- 30 Furthermore, a non-pathogenic strain of HIV-1 carries a deletion in an HIV-1-derived protein which results in an altered immunological profile. In a particularly preferred embodiment, the non-pathogenic strain of HIV-1 is substantially incapable of inducing

an antibody response to amino acids 162 to 177 to wild-type HIV-1 Nef protein. According to this preferred aspect of the present invention, there is provided a non-pathogenic HIV-1 isolate which:

- (i) induces an immune response in a human or primate subject;
- 5 (ii) does not substantially reduce proliferative responses or cytokine production to a mitogen, alloantigen and/or recall antigen relative to a healthy, non-infected subject; and
- (iii) is substantially incapable of inducing an antibody response to amino acids 162 to 177 of wild-type HIV-1 Nef protein.

10

The genomes or complementary DNA therefrom of the non-pathogenic HIV-1 isolates of the present invention are capable of hybridising under medium stringency conditions to the corresponding genome or complementary DNA of a pathogenic strain of HIV-1 (e.g. HIV-1 strain HIV-1_{NL43}). The ability to hybridize to a pathogenic strain of HIV-1
15 only applies to a comparison of the entire genome/complementary DNA of a non-pathogenic strain or a fragment which includes genetic material corresponding to a region in the genome 3' of the *nef* gene in a pathogenic strain of HIV-1.

Reference herein to "wild-type HIV-1" is meant to include reference to architypal
20 pathogenic strain HIV-1_{NL43} (Myers *et al*, 1992; 1994). For the purposes of reference only, a suitable genomic nucleotide sequence from HIV-1_{NL43} is set forth in SEQ ID NO: 1 (Myers *et al*, 1992; 1994):

```

1  TGGAAGGGCTAATTGGTCCCAAAAAGACAAGAGATCCTTGATCTGTGG
51  ATCTACCACACACAAGGCTACTTCCCTGATTGCCAGAACTACACACCAGG
25  101  GCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTTCAAGTTAGTAC
151  CAGTTGAACCAGAGCAAGTAGAAGAGGCCAAATAAGGAGAGAAGAACAGC
201  TTGTTACACCCTATGAGCCAGCATGGGATGGAGGACCCGGAGGGAGAAGT
251  ATTAGTGTGGAAGTTTGACAGCCTCCTAGCATTTCGTACATGGCCCGAG
301  AGCTGCATCCGGAGTACTACAAAGACTGCTGACATGGAGCTTTCTACAAG
30  351  GGACTTTCGGCTGGGGACTTTCCAGGGAGGTGTGGCCTGGGCCGGGACTGG
401  GGAGTGGCGAGCCCTCAGATGCTACATATAAGCAGCTGCTTTTTGCCCTGT
451  ACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTA
501  ACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCCTTGAGTGCTCA
551  AAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTC

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601 AGACCCCTTTTAGTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGG
651 GACTTGAAAGCGAAAGTAAAGCCAGAGGAGATCTCTCGACGCAGGACTCG
701 GCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGCGACTGGTGAGTA
751 CGCCAAAAATTTTACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAG
5 801 AGCGTCGGTATTAAGCGGGGGAGAATTAGATAAAATGGGAAAAAATTCGGT
851 TAAGGCCAGGGGGAAAGAAACAATATAAACTAAAACATATAGTATGGGCA
901 AGCAGGGAGCTAGAACGATTTCGCAGTTAATCCTGGCCCTTTTAGAGACATC
951 AGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAG
1001 GATCAGAAGAACTTAGATCATTATATAATACAATAGCAGTCCCTCTATTGT
10 1051 GTGCATCAAAGGATAGATGTAAAAGACACCAAGGAAGCCTTAGATAAGAT
1101 AGAGGAAGAGCAAAACAAAAGTAAGAAAAAGGCACAGCAAGCAGCAGCTG
1151 ACACAGGAAACAACAGCCAGGTCAAGCCAAAATTACCTTATAGTGCAGAAC
1201 CTCCAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGC
1251 ATGGGTAAAAGTAGTAGAAGAGAAGGCTTTTCAGCCCAGAAAGTAATACCCA
15 1301 TGTTTTTCAGCATTATCAGAAGGAGCCACCCCAAGATTTAAATACCATG
1351 CTAAACACAGTGGGGGGACATCAAGCAGCCATGCAATGTAAAAGAGAC
1401 CATCAATGAGGAAGCTGCAGAAATGGGATAGATTGCATCCAGTGCATGCAG
1451 GGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCA
1501 GGAECTACTAGTACCCTTCAGGAACAAATAGGATGGATGACACATAATCC
20 1551 ACCTATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAA
1601 ATAAATAGTAAGAATGTATAGCCCTACCAGCATTCTGGACATAAGACAA
1651 GGACCAAAGGAACCCCTTTAGAGACTATGTAGACCGATTCTATAAACTCT
1701 AAGAGCCGAGCAAGCTTCACAAGAGGTAAAAAATTGGATGACAGAAACCT
1751 TGTGTTCCAAAATGCGAACCCAGATTGTAAGACTATTTTAAAAGCATTG
25 1801 GGACCAGGAGCGACACTAGAAGAAATGATGACAGCATGTCAAGGAGTGGG
1851 GGGACCCGGCCATAAAGCAAGAGTTTTTGGCTGAAGCAATGAGCCAAAGTAA
1901 CAAATCCAGCTACCATAATGATACAGAAAGGCAATTTTAGGAACCAAAGA
1951 AAGACTGTTAAGTGTTCATTGTGGCAAAGAAGGGCACATAGCCAAAAA
2001 TTGCAGGGCCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGAAAGGAAGGAC
30 2051 ACCAAATGAAAGATTGTACTGAGAGACAGGCTAATTTTTTAGGGAAGATC
2101 TGGCCTTCCACAAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGA
2151 GCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAAGAGACAACAA
2201 CTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAAGTGTATCCTTTAGCT
2251 TCCCTCAGATCACTCTTTGGCAGCGACCCCTCGTCACAATAAGATAGGG
35 2301 GGGCAATTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATT
2351 AGAAGAAATGAATTTGCCAGGAAGATGGAAACCAAAAATGATAGGGGGAA
2401 TTGGAGGTTTTATCAAAGTAGGACAGTATGATCAGATACTCATAGAAATC
2451 TGCGGACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAA

2501 CATAATTGGAAGAAATCTGTTGACTCAGATTGGCTGCACTTTAAATTTTC
2551 CCATTAGTCCTATTGAGACTGTACCAGTAAAATTAAAGCCAGGAATGGAT
2601 GGCCCAAAAGTTAAACAATGGCCATTGACAGAAAGAAAAATAAAAGCATT
2651 AGTAGAAATTTGTACAGAAATGGAAAAGGAAGGAAAAATTTCAAAAATTG
5 2701 GGCCTGAAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAGAC
2751 AGTACTAAATGGAGAAAATTAGTAGATTTTCAGAGAACTTAATAAGAGAAC
2801 TCAAGATTTCTGGGAAGTTCAATTAGGAATACCACATCCTGCAGGGTTAA
2851 AACAGAAAAAATCAGTAACAGTACTGGATGTGGGCGATGCATATTTTCA
2901 GTTCCCTTAGATAAAGACTTCAGGAAGTATACTGCATTTTACCATACCTAG
10 2951 TATAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGCTTCCAC
3001 AGGGATGGAAAGGATCACCAGCAATATTCCAGTGTAGCATGACAAAAATC
3051 TTAGAGCCTTTTAGAAAACAAAATCCAGACATAGTCATCTATCAATACAT
3101 GGATGATTTGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAA
3151 AAATAGAGGAACTGAGACAACATCTGTTGAGGTGGGGATTTACCACACCA
15 3201 GACAAAAACATCAGAAAGAACCTCCATTCTTTGGATGGGTTATGAACT
3251 CCATCCTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAGGACA
3301 GCTGGACTGTCAATGACATACAGAAATTAGTGGGAAAATTGAATTGGGCA
3351 AGTCAGATTTATGCAGGGATTAAAGTAAGGCAATTATGTAACTTCTTAG
3401 GGGAACCAAAGCACTAACAGAAGTAGTACCCTAACAGAAAGAACAGAGC
20 3451 TAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCGGTACATGGAGTG
3501 TATTATGACCCATCAAAGACTTAATAGCAGAAATACAGAAAGCAAGGGCA
3551 AGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAA
3601 CAGGAAAATATGCAAGAATGAAGGGTGCCCACTAATGATGTGAACAA
3651 TTAACAGAGGCAGTACAAAAAATAGCCACAGAAAGCATAGTAATATGGGG
25 3701 AAAGACTCCTAAATTTAAATTACCCATACAAAAGGAACATGGGAAGCAT
3751 GGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGTGTC
3801 AATACCCCTCCCTTAGTGAAGTTATGGTACCAATTAGAGAAAGAACCCAT
3851 AATAGGAGCAGAACTTTCTATGTAGATGGGGCAGCCAATAGGGAACTA
3901 AATTAGGAAAAGCAGGATATGTAACTGACAGAGGAAGACAAAAGTTGTGTC
30 3951 CCCCTAACGGACACAACAAATCAGAAGACTGAGTTACAAGCAATTCATCT
4001 AGCTTTGCAGGATTCGGGATTAGAAGTAAACATAGTGACAGACTCACAAT
4051 ATGCATTGGGAATCATTCAAGCACAAACCAGATAAGAGTGAATCAGAGTTA
4101 GTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAAGTCTACCTGGC
4151 ATGGGTACCAGCACAAAGGAATTGGAGGAAATGAACAAAGTAGATGGGT
35 4201 TGGTCAGTGCTGGAATCAGGAAAGTACTATTTTATAGATGGAATAGATAAG
4251 GCCCAAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAG
4301 TGATTTTAACTTACCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTG
4351 ATAAATGTCAGCTAAAAGGGGAAGCCATGCATGGACAAGTAGACTGTAGC

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4401 CCAGGAATATGGCAGCTAGATTGTACACATTTAGAAGGAAAAGTTATCTT
4451 GGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAAGTAATTCCAG
4501 CAGAGACAGGGCAAGAAACAGCATACTTCTCTTAAATTTAGCAGGAAGA
4551 TGGCCAGTAAAAACAGTACATACAGACAATGGCAGCAATTTCCACCAGTAC
5 4601 TACAGTTAAGGCCGCTGTGTTGGTGGGCGGGGATCAAGCAGGAATTTGGCA
4651 TTCCCTACAATCCCCAAAGTCAAGGAGTAATAGAATCTATGAATAAAGAA
4701 TTAAAGAAAATTATAGGACAGGTAAGAGATCAGGCTGAACATCTTAAGAC
4751 AGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGA
4801 TTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGAC
10 4851 ATACAACTAAAGAATTACAAAAACAAATTACAAAATTCMAAATTTTCG
4901 GGTTTATTACAGGGACAGCAGAGATCCAGTTTGGAAAGGACCAGCAAGC
4951 TCCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAAGATAATAGTGACATA
5001 AAAGTAGTGCCAAGAAGAAAAGCAAAGATCATCAOGGATTATGGAAAACA
5051 GATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAACACA
15 5101 TGGAAAAGATTAGTAAACACCCATATGTATATTTCAAGGAAAGCTAAGGA
5151 CTGGTTTTATAGACATCACTATGAAAGTACTAATCCAAAAATAAGTTTCAG
5201 AAGTACACATCCCCTAGGGGATGCTAAATTAGTAATAACAACATATTGG
5251 GGTCTGCATACAGGAGAAAGAGACTGGCATTGGGTGAGGAGTCTCCAT
5301 AGAATGGAGGAAAAAGAGATATAGCACACAAGTAGACCCTGACCTAGCAG
20 5351 ACCAACTAATTCATCTGCACTATTTTGATTGTTTTTCAGAATCTGCTATA
5401 AGAAATACCATATTAGGACGTATAGTTAGTCCTAGGTGTGAATATCAAGC
5451 AGGACATAACAAGGTAGGATCTCTACAGTACTTGGCACTAGCAGCATTAA
5501 TAAAACCAAAACAGATAAAGCCACCTTTGCCCTAGTGTTAGGAACTGACA
5551 GAGGACAGATGGAAACAAGCCCCAGAAGACCAAGGGCCACAGAGGGAGCCA
25 5601 TACAATGAATGGACACTAGAGCTTTTAGAGGAACTTAAGAGTGAAGCTGT
5651 TAGACATTTTCTAGGATATGGCTCCATAACTTAGGACAACATATCTATG
5701 AAACCTACGGGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAAATCTG
5751 CAACAACCTGCTGTTTATCCATTTCAGAATTGGGTGTGACATAGCAGAAT
5801 AGGCGTTACTCGACAGAGGAGAGCAAGAAATGGAGCCAGTAGATCCTAGA
30 5851 CTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACCTGCTTGTACCAA
5901 TTGCTATTGTAAAAAGTGTGCTTTCATTGCCAAGTTTGTTCATGACAA
5951 AAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGA
6001 GCTCATCAGAACAGTCAGACTCATCAAGCTTCTCTATCAAGCAGTAAGT
6051 AGTACATGTAATGCAACCTATAATAGTAGCAATAGTAGCATTAGTAGTAG
35 6101 CAATAATAATAGCAATAGTTGTGTGGTCCATAGTAATCATAGAATATAGG
6151 AAAATATTAAGACAAAGAAAAATAGACAGGTTAATTGATAGACTAATAGA
6201 AAGAGCAGAAGACAOTGGCAATGAGAGTGAAGGAGAAGTATCAGCACTTG
6251 TGGAGATGGGGGTGGAAATGGGGCACCATGCTCCTTGGGATATTGATGAT

6301 CTGTAGTGCTACAGAAAAATTGTGGGTCACAGTCTATTATGGGGTACCTG
6351 TGTGGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCA
6401 TATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCAC
6451 AGACCCCAACCCACAAGAAGTAGTATTGGTAAATGTGACAGAAAAATTTTA
5 6501 ACATGTGGAAAAATGACATGGTAGAACAGATGCATGAGGATATAATCAGT
6551 TTATGGGATCAAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGT
6601 TAGTTTAAAGTGCACCTGATTTGAAGAATGATACTAATACCAATAGTAGTA
6651 GCGGGAGAATGATAATGGAGAAAGGAGAGATAAAAACTGCTCTTTCAAT
6701 ATCAGCACAAGCATAAGAGATAAGGTGCAGAAAGAATATGCATTCTTTTA
10 6751 TAACTTGATATAGTACCAATAGATAATACCAOCTATAGGTTGATAAGTT
6801 GTAACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAGCCA
6851 ATTCCCATACATTATTGTGCCCGGCTGGTTTTGCGATTCTAAAATGTAA
6901 TAATAAGACGTTCAATGGAACAGGACCATGTACAAATGTCAGCACAGTAC
6951 AATGTACACATGGAATCAGGCCAGTAGTATCAACTCAACTGCTGTTAAAT
15 7001 GGCAGTCTAGCAGAAGAAGATGTAGTAATTAGATCTGCCAATTTACAGA
7051 CAATGCTAAAACCATAATAGTACAGCTGAACACATCTGTAGAAATTAATT
7101 GTACAAGACCCAACAACAATACAGAAAAAGTATCCGTATCCAGAGGGGA
7151 CCAGGGAGAGCATTGTGTACAATAGGAAAAATAGGAAATATGAGACAAGC
7201 ACATTGTAACATTAGTAGAGCAAAATGGAATGCCACTTTAAAACAGATAG
20 7251 CTAGCAAATTAAGAGAACAATTTGGAAATAATAAAACAATAATCTTTAAG
7301 CAATCCTCAGGAGGGGACCCAGAAATTGTAACGCACAGTTTTAATTGTGG
7351 AGGGGAATTTTCTACTGTAATTCAACACAACCTGTTTAATAGTACTTGGT
7401 TTAATAGTACTTGGAGTACTGAAGGGTCAAATAACACTGAAGGAAGTGAC
7451 ACAATCACACTCCCATGCAGAATAAAACAATTTATAAACATGTGGCAGGA
25 7501 AGTAGGAAAAGCAATGTATGCCCCCTCCCATCAGTGGACAAATTAGATGTT
7551 CATCAAATATTACTGGGCTGCTATTAACAAGAGATGGTGGTAATAACAAC
7601 AATGGGTCCGAGATCTTCAGACCTGGAGGAGGCGATATGAGGGACAATTG
7651 GAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAG
7701 TAGCACCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAGAGCA
30 7751 GTGGGAATAGGAGCTTTGTTCTTGGGTTCTTGGGAGCAGCAGGAAGCAC
7801 TATGGGCTGCACGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGT
7851 CTGATATAGTGCAGCAGCAGAACAATTTGCTGAGGCTATTGAGGCGCAA
7901 CAGCATCTGTTGCAACTCACAGTCTGGGGCATCAACAGCTCCAGGCAAG
7951 AATCCTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTT
35 8001 GGGGTTGCTCTGGAAAACTCATTTCACCACTGCTGTGCCTTGGAATGCT
8051 AGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATAACATGACCTGGAT
8101 GGAGTGGGACAGAGAAATTAACAATTACACAAGCTTAATACACTCCTTAA
8151 TTGAAGAATCGCAAAACCAGCAAGAAAGAATGAACAAGAATTATTGGAA

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- 26 -

8201 TTAGATAAATGGGCAAGTTTGTGGAATTGGTTTAAACATAACAAATTGGCT
 8251 GTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAA
 8301 GAATAGTTTTTGTCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATAT
 8351 TCACCATTATCGTTTCAGACCCACCTCCCAATCCCGAGGGGACCCGACAG
 5 8401 GCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCA
 8451 TTCGATTAGTGAACGGATCCTTAGCACTTATCTGGGACGATCTGCGGAGC
 8501 CTGTGCCCTCTTCAGCTACCACCGCTTGAGAGACTTACTCTTGATTGTAAC
 8551 GAGGATTGTGGAACCTTCTGGGACGACAGGGGTGGGAAGCCCTCAAATATT
 8601 GGTGGAATCTCCTACAGTATTGGAATCAGGAATAAAGAAATAGTGCTGTT
 10 8651 AACTTGCTCAATGCCACAGCCATAACAGTAGCTGAGGGGACAGATAGGGT
 8701 TATAGAAGTATTACAAGCAGCTTATAGAGCTATTGCCACATACCTAGAA
 8751 GAATAAGACAGGGCTTGGAAGGATTTTGCTATAAGATGGGTGGCAAGTG
 8801 GTCAAAAAGTAGTGTGATTGGATGGCCTGCTGTAAAGGAAAGAAATGAGAC
 8851 GAGCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTGAGACCTAGAA
 15 8901 AAACATGGAGCAATCACAAGTAGCAATACAGCAGCTAACAAATGCTGCTTG
 8951 TGCCTGGCTAGAAGCACAGAGGAGGAAGAGGTGGGTTTTCCAGTCACAC
 9001 CTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGC
 9051 CACTTTTTTAAAGAAAAGGGGGGACTGGAAGGGCTAATTCCTCCCAAAG
 9101 AAGACAAGATATCCTTGATCTGTGATCTACCACACACAAAGGCTACTTCC
 20 9151 CTGATTGGCAGAACTACACACCAGGGCCAGGGGTCAATATCCACTGACC
 9201 TTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGA
 9251 GGCCAATAAAGGAGAGAAACACCAGCTTGTTACACCCTGTGAGCCTGCATG
 9301 GAATGGATGACCCTGAGAGAGAAAGTGTAGAGTGGAGGTTTGACAGCCGC
 9351 CTAGCATTTTCATCACGTGGCCCCGAGAGCTGCATCCGAGTACTTCAAGAA
 25 9401 CTGCTGACATCGAGCTTGCTACAAGGGACTTTCCGCTGGGAGCTTTCCAG
 9451 GGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGATGCTGC
 9501 ATATAAGCAGCTGCTTTTTGCTGTACTGGGTCTCTCTGTTAGACCAGA
 9551 TCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAAACCCACTGCTTAAGCCT
 9601 CAATAAAGCTTGCCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTG
 30 9651 TGA CTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAAGTGTGGAAAA
 9701 TCTCTAGCA

However, for the purposes of comparing the nucleotide sequences of non-pathogenic
 HIV-1 strains including the ability to hybridize to a reference strain, the present
 35 invention extends to a genomic nucleotide sequence from any pathogenic strain of HIV-
 1.

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- 27 -

Reference to a biological source includes blood or blood-related products or components such as lymphocytes, plasma, tissue fluid and tissue extracts.

Accordingly, in a particularly preferred embodiment, there is provided a viral isolate

5 which:

- (i) carries a genome which is capable of hybridising under medium stringency conditions to SEQ ID NO: 1 or a complementary form thereof or an analogous sequence from another pathogenic strain of HIV-1; and
- (ii) carries a deletion mutation in a region corresponding to the *nef* gene and/or in
10 an LTR region. Generally, such an HIV-1 isolate is non-pathogenic as hereinbefore defined.

In a related embodiment, there is provided an isolated virus which:

- (i) has a genome which is capable of hybridising under medium stringency
15 conditions to complementary nucleic acid from a pathogenic strain of HIV-1; and
- (ii) carries one or more deletion mutations in a region of its genome corresponding to a region which contains *nef* coding sequences and LTR nucleotide sequences.

20 For the purposes of defining the level of stringency, reference can conveniently be made to Maniatis *et al* (1982) at pages 387-389 which is herein incorporated by reference where the washing steps disclosed are considered high stringency. A low stringency is defined herein as being in 1-3X SSC/0.1-0.5% w/v SDS at 37-50°C for 2-3 hours. Depending on the source and concentration of nucleic acid involved in the hybridisation,
25 alternative conditions of stringency may be employed such as medium stringent conditions which are considered herein to be 0.1-1X SSC/0.25-0.5% w/v SDS at $\geq 45^{\circ}\text{C}$ for 2-3 hours or high stringent conditions considered herein to be 0.1-1X SSC/0.1% w/v SDS at 60°C for 1-3 hours.

30 In a particularly preferred embodiment of the present invention, the non-pathogenic strain of HIV-1 carries a mutation in the *nef* gene and/or LTR region of the genome.

- 28 -

In an even more preferred embodiment, the non-pathogenic strain of HIV-1 carries a mutation in the *nef* gene such that a Nef protein is not produced or a modified Nef protein is produced substantially not carrying amino acids 162 to 177 or a portion thereof from wild-type Nef.

5

A "mutation" is considered herein to include a single or multiple nucleotide substitution, deletion and/or addition. Most preferred mutations are single or multiple deletions of at least one, most preferably at least ten and even more preferably at least twenty contiguous nucleotides from a region corresponding to the *nef* gene and/or the LTR
10 region. When the non-pathogenic virus carries a mutation in the LTR region, this generally occurs 5' of the *Sp1* sites. A particularly preferred deletion is from a region within the *nef* gene corresponding to amino acids 162 to 177 of the Nef protein.

According to a preferred aspect of the present invention, there is provided a viral isolate
15 which:

- (i) is reactive to antibodies to a glycoprotein from HIV-1 such as at least one of gp41-45, gp120 and/or gp160;
- (ii) is substantially non-pathogenic in human subjects; and
- (iii) carries a deletion mutation of at least ten nucleotides in a region corresponding
20 to the *nef* gene and/or LTR region of a pathogenic strain of HIV-1.

In another embodiment, there is provided a viral isolate which:

- (i) is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env*;
- (ii) is substantially non-pathogenic in human subjects; and
- 25 (iii) carries a deletion mutation of at least ten nucleotides in a region corresponding to the *nef* gene and/or LTR region of a pathogenic strain of HIV-1.

Preferably, in respect of the latter embodiment, the immune response is an antibody or a cell mediated response. In a most preferred embodiment, the immune response is a
30 humoral immune response.

In another aspect of the present invention, there is provided a viral isolate which:

- (i) is interactive to antibodies to a glycoprotein from HIV-1 such as at least one of gp41-45, gp120 and/or gp160;
- 5 (ii) is substantially non-pathogenic in human subjects; and
- (iii) carries a deletion mutation of at least ten nucleotides in a region corresponding to all or part of amino acids 162 to 177 encoded by the *nef* gene of a pathogenic strain of HIV-1.

- 10 The nucleotide sequence of the *nef* gene in HIV-1_{NL43} is defined in SEQ ID NO: 650:
 ATGGGTGGCAAGTGGTCAAAAAGTAGTGTGATTGGATGGCCTGCTGTAAGGGAAAGAAT
 GAGACGAGCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTAGAAAAAC
 ATGGAGCAATCACAAGTAGCAATACAGCAGCTAACAATGCTGCTTGTGCCTGGCTAGAA
 GCACAAGAGGAGGAAGAGGTGGGTTTTCAGTCACACCTCAGGTACCTTTAAGACCAAT
 15 GACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAG
 GGCTAATTCACCTCCCAAGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAA
 GGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTCAGATATCCACTGAC
 CTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAGGCCAATA
 AAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAG
 20 AGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCTAGCATTTCATCAAGTGGCCCGAGA
 GCTGCATCCGGAGTACTTCAAGAACTGCTGA

The nucleotide sequence encoding amino acids 162-177 of wild-type HIV-1_{NL43} Nef is as follows:

- 25 ACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAG [SEQ ID NO: 802].

- The present invention extends to any or all single or multiple nucleotide deletions to a contiguous series of at least ten nucleotides from the *nef* gene which render the strain
 30 avirulent. The deletions may encompass the entire gene or parts thereof and may represent a single deletion or two or more deletions. Put in alternative terms, the non-pathogenic HIV-1 isolates of the present invention comprise a nucleotide sequence at the corresponding *nef* gene region non-identifiable to SEQ ID NO: 650, said non-identity comprising at least 5%, more preferably at least 10% and even more preferably at least

20% variation thereon. The present invention particularly extends to any or all single or multiple nucleotide deletions to a contiguous series of at least ten nucleotides from the region of the *nef* gene corresponding to all or part of amino acids 162 to 177 and which render the strain avirulent. Although this aspect of the present invention is exemplified by specific reference to amino acids 162 to 177, the present invention also extends to a functionally analogous sequence where, for example, amino acids are substituted by structurally or functionally similar amino acids. In addition, the present invention extends to any deletion or other mutation in an HIV-1 derived protein which renders that strain non-pathogenic.

10

In a preferred embodiment, therefore, the present invention contemplates a viral isolate which:

- (i) is reactive to antibodies to a glycoprotein from HIV-1 such as at least one of gp41-45, gp120 and/or gp160;
- 15 (ii) carries a genome or a part or fragment thereof capable of hybridising under medium stringency conditions to a nucleotide sequence as set forth in SEQ ID NO: 1 or a complementary form thereof or an analogous sequence from another pathogenic strain of HIV-1;
- (iii) carries a deletion of at least ten nucleotides in a region corresponding to the *nef* gene in HIV-1_{NL43}; and

20

wherein said deletion encompasses one or more of the following decanucleotides from the *nef* gene of HIV-1_{NL43} or corresponding sequences from another pathogenic strain of HIV-1:

- | | |
|--------------------------------|-----------------------------|
| ATGGGTGGCA (SEQ ID NO: 2); | TGGGTGGCAA (SEQ ID NO: 3); |
| 25 GGTGGCAAG (SEQ ID NO: 4); | GGTGGCAAGT (SEQ ID NO: 5); |
| GTGGCAAGTG (SEQ ID NO: 6); | TGGCAAGTGG (SEQ ID NO: 7); |
| GGCAAGTGGT (SEQ ID NO: 8); | GCAAGTGGTC (SEQ ID NO: 9); |
| CAAGTGGTCA (SEQ ID NO: 10); | AAGTGGTCAA (SEQ ID NO: 11); |
| AGTGGTCAAA (SEQ ID NO: 12); | GTGGTCAAAA (SEQ ID NO: 13); |
| 30 TGGTCAAAAA (SEQ ID NO: 14); | GGTCAAAAAG (SEQ ID NO: 15); |
| GTCAAAAAGT (SEQ ID NO: 16); | TCAAAAAGTA (SEQ ID NO: 17); |
| CAAAAAGTAG (SEQ ID NO: 18); | AAAAAGTAGT (SEQ ID NO: 19); |
| AAAAGTAGTG (SEQ ID NO: 20); | AAAGTAGTGT (SEQ ID NO: 21); |
| AAGTAGTGTG (SEQ ID NO: 22); | AGTAGTGTGA (SEQ ID NO: 23); |

	GTAGTGTGAT (SEQ ID NO: 24);	TAGTGTGATT (SEQ ID NO: 25);
	AGTGTGATTG (SEQ ID NO: 26);	GTGTGATTGG (SEQ ID NO: 27);
	TGTGATTGGA (SEQ ID NO: 28);	GTGATTGGAT (SEQ ID NO: 29);
	TGATTGGATG (SEQ ID NO: 30);	GATTGGATGG (SEQ ID NO: 31);
5	ATTGGATGGC (SEQ ID NO: 32);	TTGGATGGCC (SEQ ID NO: 33);
	TGGATGGCCT (SEQ ID NO: 34);	GGATGGCCTG (SEQ ID NO: 35);
	GATGGCCTGC (SEQ ID NO: 36);	ATGGCCTGCT (SEQ ID NO: 37);
	TGGCCTGCTG (SEQ ID NO: 38);	GGCCTGCTGT (SEQ ID NO: 39);
	GCCTGCTGTA (SEQ ID NO: 40);	CCTGCTGTAA (SEQ ID NO: 41);
10	CTGCTGTAAG (SEQ ID NO: 42);	TGCTGTAAGG (SEQ ID NO: 43);
	GCTGTAAGGG (SEQ ID NO: 44);	CTGTAAGGGA (SEQ ID NO: 45);
	TGTAAGGGAA (SEQ ID NO: 46);	GTAAGGGAAA (SEQ ID NO: 47);
	TAAGGGAAAG (SEQ ID NO: 48);	AAGGGAAAGA (SEQ ID NO: 49);
	AGGGAAAGAA (SEQ ID NO: 50);	GGGAAAGAAT (SEQ ID NO: 51);
15	GGAAAGAATG (SEQ ID NO: 52);	GAAAGAATGA (SEQ ID NO: 53);
	AAAGAATGAG (SEQ ID NO: 54);	AAGAATGAGA (SEQ ID NO: 55);
	AGAATGAGAC (SEQ ID NO: 56);	GAATGAGACG (SEQ ID NO: 57);
	AATGAGACGA (SEQ ID NO: 58);	ATGAGACGAG (SEQ ID NO: 59);
	TGAGACGAGC (SEQ ID NO: 60);	GAGACGAGCT (SEQ ID NO: 61);
20	AGACGAGCTG (SEQ ID NO: 62);	GACGAGCTGA (SEQ ID NO: 63);
	ACGAGCTGAG (SEQ ID NO: 64);	CGAGCTGAGC (SEQ ID NO: 65);
	GAGCTGAGCC (SEQ ID NO: 66);	AGCTGAGCCA (SEQ ID NO: 67);
	GCTGAGCCAG (SEQ ID NO: 68);	CTGAGCCAGC (SEQ ID NO: 69);
	TGAGCCAGCA (SEQ ID NO: 70);	GAGCCAGCAG (SEQ ID NO: 71);
25	AGCCAGCAGC (SEQ ID NO: 72);	GCCAGCAGCA (SEQ ID NO: 73);
	CCAGCAGCAG (SEQ ID NO: 74);	CAGCAGCAGA (SEQ ID NO: 75);
	AGCAGCAGAT (SEQ ID NO: 76);	GCAGCAGATG (SEQ ID NO: 77);
	CAGCAGATGG (SEQ ID NO: 78);	AGCAGATGGG (SEQ ID NO: 79);
	GCAGATGGGG (SEQ ID NO: 80);	CAGATGGGGT (SEQ ID NO: 81);
30	AGATGGGGTG (SEQ ID NO: 82);	GATGGGGTGG (SEQ ID NO: 83);
	ATGGGGTGGG (SEQ ID NO: 84);	TGGGGTGGGA (SEQ ID NO: 85);
	GGGGTGGGAG (SEQ ID NO: 86);	GGGTGGGAGC (SEQ ID NO: 87);
	GGTGGGAGCA (SEQ ID NO: 88);	GTGGGAGCAG (SEQ ID NO: 89);
	TGGGAGCAGT (SEQ ID NO: 90);	GGGAGCAGTA (SEQ ID NO: 91);
35	GGAGCAGTAT (SEQ ID NO: 92);	GAGCAGTATC (SEQ ID NO: 93);
	AGCAGTATCT (SEQ ID NO: 94);	GCAGTATCTC (SEQ ID NO: 95);
	CAGTATCTCG (SEQ ID NO: 96);	AGTATCTCGA (SEQ ID NO: 97);
	GTATCTCGAG (SEQ ID NO: 98);	TATCTCGAGA (SEQ ID NO: 99);

ATCTCGAGAC (SEQ ID NO: 100); TCTCGAGACC (SEQ ID NO: 101);
CTCGAGACCT (SEQ ID NO: 102); TCGAGACCTA (SEQ ID NO: 103);
CGAGACCTAG (SEQ ID NO: 104); GAGACCTAGA (SEQ ID NO: 105);
AGACCTAGAA (SEQ ID NO: 106); GACCTAGAAA (SEQ ID NO: 107);
5 ACCTAGAAAA (SEQ ID NO: 108); CCTAGAAAAA (SEQ ID NO: 109);
CTAGAAAAAC (SEQ ID NO: 110); TAGAAAAACA (SEQ ID NO: 111);
AGAAAAACAT (SEQ ID NO: 112); GAAAAACATG (SEQ ID NO: 113);
AAAAACATGG (SEQ ID NO: 114); AAAACATGGA (SEQ ID NO: 115);
AAACATGGAG (SEQ ID NO: 116); AACATGGAGC (SEQ ID NO: 117);
10 ACATGGAGCA (SEQ ID NO: 118); CATGGAGCAA (SEQ ID NO: 119);
ATGGAGCAAT (SEQ ID NO: 120); TGGAGCAATC (SEQ ID NO: 121);
GGAGCAATCA (SEQ ID NO: 122); GAGCAATCAC (SEQ ID NO: 123);
AGCAATCACA (SEQ ID NO: 124); GCAATCACAA (SEQ ID NO: 125);
CAATCACAAG (SEQ ID NO: 126); AATCACAAGT (SEQ ID NO: 127);
15 ATCACAAGTA (SEQ ID NO: 128); TCACAAGTAG (SEQ ID NO: 129);
CACAAGTAGC (SEQ ID NO: 130); ACAAGTAGCA (SEQ ID NO: 131);
CAAGTAGCAA (SEQ ID NO: 132); AAGTAGCAAT (SEQ ID NO: 133);
AGTAGCAATA (SEQ ID NO: 134); GTAGCAATAC (SEQ ID NO: 135);
TAGCAATACA (SEQ ID NO: 136); AGCAATACAG (SEQ ID NO: 137);
20 GCAATACAGC (SEQ ID NO: 138); CAATACAGCA (SEQ ID NO: 139);
AATACAGCAG (SEQ ID NO: 140); ATACAGCAGC (SEQ ID NO: 141);
TACAGCAGCT (SEQ ID NO: 142); ACAGCAGCTA (SEQ ID NO: 143);
CAGCAGCTAA (SEQ ID NO: 144); AGCAGCTAAC (SEQ ID NO: 145);
GCAGCTAACA (SEQ ID NO: 146); CAGCTAACAA (SEQ ID NO: 147);
25 AGCTAACAAAT (SEQ ID NO: 148); GCTAACAAATG (SEQ ID NO: 149);
CTAACAAATG (SEQ ID NO: 150); TAACAAATGCT (SEQ ID NO: 151);
AACAAATGCTG (SEQ ID NO: 152); ACAATGCTGCT (SEQ ID NO: 153);
CAATGCTGCT (SEQ ID NO: 154); AATGCTGCTT (SEQ ID NO: 155);
ATGCTGCTTG (SEQ ID NO: 156); TGCTGCTTGT (SEQ ID NO: 157);
30 GCTGCTTGTG (SEQ ID NO: 158); CTGCTTGTGC (SEQ ID NO: 159);
TGCTTGTGCC (SEQ ID NO: 160); GCTTGTGCCT (SEQ ID NO: 161);
CTTGTGCCTG (SEQ ID NO: 162); TTGTGCCTGG (SEQ ID NO: 163);
TGTGCCTGGC (SEQ ID NO: 164); GTGCCTGGCT (SEQ ID NO: 165);
TGCCTGGCTA (SEQ ID NO: 166); GCCTGGCTAG (SEQ ID NO: 167);
35 CCTGGCTAGA (SEQ ID NO: 168); CTGGCTAGAA (SEQ ID NO: 169);
TGGCTAGAAG (SEQ ID NO: 170); GGCTAGAAGC (SEQ ID NO: 171);
GCTAGAAGCA (SEQ ID NO: 172); CTAGAAGCAC (SEQ ID NO: 173);
TAGAAGCACA (SEQ ID NO: 174); AGAAGCACAA (SEQ ID NO: 175);

GAAGCACAAG (SEQ ID NO: 176); AAGCACAAGA (SEQ ID NO: 177);
AGCACAAGAG (SEQ ID NO: 178); GCACAAGAGG (SEQ ID NO: 179);
CACAAGAGGA (SEQ ID NO: 180); ACAAGAGGAG (SEQ ID NO: 181);
CAAGAGGAGG (SEQ ID NO: 182); AAGAGGAGGA (SEQ ID NO: 183);
5 AGAGGAGGAA (SEQ ID NO: 184); GAGGAGGAAG (SEQ ID NO: 185);
AGGAGGAAGA (SEQ ID NO: 186); GGAGGAAGAG (SEQ ID NO: 187);
GAGGAAGAGG (SEQ ID NO: 188); AGGAAGAGGT (SEQ ID NO: 189);
GGAAGAGGTG (SEQ ID NO: 190); GAAGAGGTGG (SEQ ID NO: 191);
AAGAGGTGGG (SEQ ID NO: 192); AGAGGTGGGT (SEQ ID NO: 193);
10 GAGGTGGGTT (SEQ ID NO: 194); AGGTGGGTTT (SEQ ID NO: 195);
GGTGGGTTTT (SEQ ID NO: 196); GTGGGTTTTTC (SEQ ID NO: 197);
TGGGTTTTTCC (SEQ ID NO: 198); GGGTTTTTCCA (SEQ ID NO: 199);
GGTTTTTCCAG (SEQ ID NO: 200); GTTTTTCCAGT (SEQ ID NO: 201);
TTTTTCCAGTC (SEQ ID NO: 202); TTTCCAGTCA (SEQ ID NO: 203);
15 TTCCAGTCAC (SEQ ID NO: 204); TCCAGTCACA (SEQ ID NO: 205);
CCAGTCACAC (SEQ ID NO: 206); CAGTCACACC (SEQ ID NO: 207);
AGTCACACCT (SEQ ID NO: 208); GTCACACCTC (SEQ ID NO: 209);
TCACACCTCA (SEQ ID NO: 210); CACACCTCAG (SEQ ID NO: 211);
ACACCTCAGG (SEQ ID NO: 212); CACCTCAGGT (SEQ ID NO: 213);
20 ACCTCAGGTA (SEQ ID NO: 214); CCTCAGGTAC (SEQ ID NO: 215);
CTCAGGTACC (SEQ ID NO: 216); TCAGGTACCT (SEQ ID NO: 217);
CAGGTACCTT (SEQ ID NO: 218); AGGTACCTTT (SEQ ID NO: 219);
GGTACCTTTA (SEQ ID NO: 220); GTACCTTTAA (SEQ ID NO: 221);
TACCTTTAAG (SEQ ID NO: 222); ACCTTTAAGA (SEQ ID NO: 223);
25 CCTTTAAGAC (SEQ ID NO: 224); CTTTAAGACC (SEQ ID NO: 225);
TTTAAGACCA (SEQ ID NO: 226); TTAAGACCAA (SEQ ID NO: 227);
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AGACCAATGA (SEQ ID NO: 230); GACCAATGAC (SEQ ID NO: 231);
ACCAATGACT (SEQ ID NO: 232); CCAATGACTT (SEQ ID NO: 233);
30 CAATGACTTA (SEQ ID NO: 234); AATGACTTAC (SEQ ID NO: 235);
ATGACTTACA (SEQ ID NO: 236); TGACTTACAA (SEQ ID NO: 237);
GACTTACAAG (SEQ ID NO: 238); ACTTACAAGG (SEQ ID NO: 239);
CTTACAAGGC (SEQ ID NO: 240); TTACAAGGCA (SEQ ID NO: 241);
TACAAGGCAG (SEQ ID NO: 242); ACAAGGCAGC (SEQ ID NO: 243);
35 CAAGGCAGCT (SEQ ID NO: 244); AAGGCAGCTG (SEQ ID NO: 245);
AGGCAGCTGT (SEQ ID NO: 246); GGCAGCTGTA (SEQ ID NO: 247);
GCAGCTGTAG (SEQ ID NO: 248); CAGCTGTAGA (SEQ ID NO: 249);
AGCTGTAGAT (SEQ ID NO: 250); GCTGTAGATC (SEQ ID NO: 251);

CTGTAGATCT (SEQ ID NO: 252); TGTAGATCTT (SEQ ID NO: 253);
 GTAGATCTTA (SEQ ID NO: 254); TAGATCTTAG (SEQ ID NO: 255);
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 ATCTTAGCCA (SEQ ID NO: 258); TCTTAGCCAC (SEQ ID NO: 259);
 5 CTTAGCCACT (SEQ ID NO: 260); TTAGCCACTT (SEQ ID NO: 261);
 TAGCCACTTT (SEQ ID NO: 262); AGCCACTTTT (SEQ ID NO: 263);
 GCCACTTTTT (SEQ ID NO: 264); CCACTTTTTA (SEQ ID NO: 265);
 CACTTTTTAA (SEQ ID NO: 266); ACTTTTTAAA (SEQ ID NO: 267);
 CTTTTTAAAA (SEQ ID NO: 268); TTTTTAAAAG (SEQ ID NO: 269);
 10 TTTTAAAAGA (SEQ ID NO: 270); TTTAAAAGAA (SEQ ID NO: 271);
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 AAGAAAAGGG (SEQ ID NO: 276); AGAAAAGGGG (SEQ ID NO: 277);
 GAAAAGGGGG (SEQ ID NO: 278); AAAAGGGGGG (SEQ ID NO: 279);
 15 AAAGGGGGGA (SEQ ID NO: 280); AAGGGGGGAC (SEQ ID NO: 281);
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 20 CTGGAAGGGC (SEQ ID NO: 290); TGGGAAGGGCT (SEQ ID NO: 291);
 GGAAGGGCTA (SEQ ID NO: 292); GAAGGGCTAA (SEQ ID NO: 293);
 AAGGGCTAAT (SEQ ID NO: 294); AGGGCTAATT (SEQ ID NO: 295);
 GGGCTAATTC (SEQ ID NO: 296); GGCTAATTCA (SEQ ID NO: 297);
 GCTAATTCAC (SEQ ID NO: 298); CTAATTCACT (SEQ ID NO: 299);
 25 TAATTCACTC (SEQ ID NO: 300); AATTCACTCC (SEQ ID NO: 301);
 ATTCACTCCC (SEQ ID NO: 302); TTCCTCCCA (SEQ ID NO: 303);
 TCACTCCCAA (SEQ ID NO: 304); CACTCCCAA (SEQ ID NO: 305);
 ACTCCCAAAG (SEQ ID NO: 306); CTCCCAAAGA (SEQ ID NO: 307);
 TCCCAAAGAA (SEQ ID NO: 308); CCCAAAGAAG (SEQ ID NO: 309);
 30 CCAAAGAAGA (SEQ ID NO: 310); CAAAGAAGAC (SEQ ID NO: 311);
 AAAGAAGACA (SEQ ID NO: 312); AAGAAGACAA (SEQ ID NO: 313);
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 GACAAGATAT (SEQ ID NO: 318); ACAAGATATC (SEQ ID NO: 319);
 35 CAAGATATCC (SEQ ID NO: 320); AAGATATCCT (SEQ ID NO: 321);
 AGATATCCTT (SEQ ID NO: 322); GATATCCTTG (SEQ ID NO: 323);
 ATATCCTTGA (SEQ ID NO: 324); TATCCTTGAT (SEQ ID NO: 325);
 ATCCTTGATC (SEQ ID NO: 326); TCCTTGATCT (SEQ ID NO: 327);

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CCTTGATCTG (SEQ ID NO: 328); CTTGATCTGT (SEQ ID NO: 329);
 TTGATCTGTG (SEQ ID NO: 330); TGATCTGTGG (SEQ ID NO: 331);
 GATCTGTGGA (SEQ ID NO: 332); ATCTGTGGAT (SEQ ID NO: 333);
 TCTGTGGATC (SEQ ID NO: 334); CTGTGGATCT (SEQ ID NO: 335);
 5 TGTGGATCTA (SEQ ID NO: 336); GTGGATCTAC (SEQ ID NO: 337);
 TGGATCTACC (SEQ ID NO: 338); GGATCTACCA (SEQ ID NO: 339);
 GATCTACCAC (SEQ ID NO: 340); ATCTACCACA (SEQ ID NO: 341);
 TCTACCACAC (SEQ ID NO: 342); CTACCACACA (SEQ ID NO: 343);
 TACCACACAC (SEQ ID NO: 344); ACCACACACA (SEQ ID NO: 345);
 10 CCACACACAA (SEQ ID NO: 346); CACACACAAG (SEQ ID NO: 347);
 ACACACAAGG (SEQ ID NO: 348); CACACAAGGC (SEQ ID NO: 349);
 ACACAAGGCT (SEQ ID NO: 350); CACAAGGCTA (SEQ ID NO: 351);
 ACAAGGCTAC (SEQ ID NO: 352); CAAGGCTACT (SEQ ID NO: 353);
 AAGGCTACTT (SEQ ID NO: 354); AGGCTACTTC (SEQ ID NO: 355);
 15 GGCTACTTCC (SEQ ID NO: 356); GCTACTTCCC (SEQ ID NO: 357);
 CTACTTCCCT (SEQ ID NO: 358); TACTTCCCTG (SEQ ID NO: 359);
 ACTTCCCTGA (SEQ ID NO: 360); CTTCCCTGAT (SEQ ID NO: 361);
 TTCCCTGATT (SEQ ID NO: 362); TCCCTGATTG (SEQ ID NO: 363);
 CCCTGATTGG (SEQ ID NO: 364); CCTGATTGGC (SEQ ID NO: 365);
 20 CTGATTGGCA (SEQ ID NO: 366); TGATTGGCAG (SEQ ID NO: 367);
 GATTGGCAGA (SEQ ID NO: 368); ATTGGCAGAA (SEQ ID NO: 369);
 TTGGCAGAAC (SEQ ID NO: 370); TGGCAGAACT (SEQ ID NO: 371);
 GGCAGAACTA (SEQ ID NO: 372); GCAGAACTAC (SEQ ID NO: 373);
 CAGAACTACA (SEQ ID NO: 374); AGAACTACAC (SEQ ID NO: 375);
 25 GAACTACACA (SEQ ID NO: 376); AACTACACAC (SEQ ID NO: 377);
 ACTACACACC (SEQ ID NO: 378); CTACACACCA (SEQ ID NO: 379);
 TACACACCAG (SEQ ID NO: 380); ACACACCAGG (SEQ ID NO: 381);
 CACACCAGGG (SEQ ID NO: 382); ACACCAGGGC (SEQ ID NO: 383);
 CACCAGGGCC (SEQ ID NO: 384); ACCAGGGCCA (SEQ ID NO: 385);
 30 CCAGGGCCAG (SEQ ID NO: 386); CAGGGCCAGG (SEQ ID NO: 387);
 AGGGCCAGGG (SEQ ID NO: 388); GGGCCAGGGG (SEQ ID NO: 389);
 GGCCAGGGGT (SEQ ID NO: 390); GCCAGGGGTC (SEQ ID NO: 391);
 CCAGGGGTCA (SEQ ID NO: 392); CAGGGGTCA (SEQ ID NO: 393);
 AGGGGTCA (SEQ ID NO: 394); GGGGTCA (SEQ ID NO: 395);
 35 GGGTCAGATA (SEQ ID NO: 396); GGTCAGATAT (SEQ ID NO: 397);
 GTCAGATATC (SEQ ID NO: 398); TCAGATATCC (SEQ ID NO: 399);
 CAGATATCCA (SEQ ID NO: 400); AGATATCCAC (SEQ ID NO: 401);
 GATATCCACT (SEQ ID NO: 402); ATATCCACTG (SEQ ID NO: 403);

00445783-090998

TATCCACTGA (SEQ ID NO: 404); ATCCACTGAC (SEQ ID NO: 405);
TCCACTGACC (SEQ ID NO: 406); CCACTGACCT (SEQ ID NO: 407);
CACTGACCTT (SEQ ID NO: 408); ACTGACCTTT (SEQ ID NO: 409);
CTGACCTTTG (SEQ ID NO: 410); TGACCTTTGG (SEQ ID NO: 411);
5 GACCTTTGGA (SEQ ID NO: 412); ACCTTTGGAT (SEQ ID NO: 413);
CCTTTGGATG (SEQ ID NO: 414); CTTTGGATGG (SEQ ID NO: 415);
TTTGGATGGT (SEQ ID NO: 416); TTGGATGGTG (SEQ ID NO: 417);
TGGATGGTGC (SEQ ID NO: 418); GGATGGTGCT (SEQ ID NO: 419);
GATGGTGCTA (SEQ ID NO: 420); ATGGTGCTAC (SEQ ID NO: 421);
10 TGGTGCTACA (SEQ ID NO: 422); GGTGCTACAA (SEQ ID NO: 423);
GTGCTACAAG (SEQ ID NO: 424); TGCTACAAGC (SEQ ID NO: 425);
GCTACAAGCT (SEQ ID NO: 426); CTACAAGCTA (SEQ ID NO: 427);
TACAAGCTAG (SEQ ID NO: 428); ACAAGCTAGT (SEQ ID NO: 429);
CAAGCTAGTA (SEQ ID NO: 430); AAGCTAGTAC (SEQ ID NO: 431);
15 AGCTAGTACC (SEQ ID NO: 432); GCTAGTACCA (SEQ ID NO: 433);
CTAGTACCAG (SEQ ID NO: 434); TAGTACCAGT (SEQ ID NO: 435);
AGTACCAGTT (SEQ ID NO: 436); GTACCAGTTG (SEQ ID NO: 437);
TACCAGTTGA (SEQ ID NO: 438); ACCAGTTGAG (SEQ ID NO: 439);
CCAGTTGAGC (SEQ ID NO: 440); CAGTTGAGCC (SEQ ID NO: 441);
20 AGTTGAGCCA (SEQ ID NO: 442); GTTGAGCCAG (SEQ ID NO: 443);
TTGAGCCAGA (SEQ ID NO: 444); TGAGCCAGAT (SEQ ID NO: 445);
GAGCCAGATA (SEQ ID NO: 446); AGCCAGATAA (SEQ ID NO: 447);
GCCAGATAAG (SEQ ID NO: 448); CCAGATAAGG (SEQ ID NO: 449);
CAGATAAGGT (SEQ ID NO: 450); AGATAAGGTA (SEQ ID NO: 451);
25 GATAAGGTAG (SEQ ID NO: 452); ATAAGGTAGA (SEQ ID NO: 453);
TAAGGTAGAA (SEQ ID NO: 454); AAGGTAGAAG (SEQ ID NO: 455);
AGGTAGAAGA (SEQ ID NO: 456); GGTAAGAAGAG (SEQ ID NO: 457);
GTAGAAGAGG (SEQ ID NO: 458); TAGAAGAGGC (SEQ ID NO: 459);
AGAAGAGGCC (SEQ ID NO: 460); GAAGAGGCCA (SEQ ID NO: 461);
30 AAGAGGCCAA (SEQ ID NO: 462); AGAGGCCAAT (SEQ ID NO: 463);
GAGGCCAATA (SEQ ID NO: 464); AGGCCAATAA (SEQ ID NO: 465);
GGCCAATAAA (SEQ ID NO: 466); GCCAATAAAG (SEQ ID NO: 467);
CCAATAAAGG (SEQ ID NO: 468); CAATAAAGGA (SEQ ID NO: 469);
AATAAAGGAG (SEQ ID NO: 470); ATAAAGGAGA (SEQ ID NO: 471);
35 TAAAGGAGAG (SEQ ID NO: 472); AAAGGAGAGA (SEQ ID NO: 473);
AAGGAGAGAA (SEQ ID NO: 474); AGGAGAGAAC (SEQ ID NO: 475);
GGAGAGAACA (SEQ ID NO: 476); GAGAGAACAC (SEQ ID NO: 477);
AGAGAACACC (SEQ ID NO: 478); GAGAACACCA (SEQ ID NO: 479);

AGAACACCAG (SEQ ID NO: 480); GAACACCAGC (SEQ ID NO: 481);
AACACCAGCT (SEQ ID NO: 482); ACACCAGCTT (SEQ ID NO: 483);
CACCAGCTTG (SEQ ID NO: 484); ACCAGCTTGT (SEQ ID NO: 485);
CCAGCTTGTT (SEQ ID NO: 486); CAGCTTGTTA (SEQ ID NO: 487);
5 AGCTTGTTAC (SEQ ID NO: 488); GCTTGTTACA (SEQ ID NO: 489);
CTTGTTACAC (SEQ ID NO: 490); TTGTTACACC (SEQ ID NO: 491);
TGTTACACCC (SEQ ID NO: 492); GTTACACCTT (SEQ ID NO: 493);
TTACACCCTG (SEQ ID NO: 494); TACACCCTGT (SEQ ID NO: 495);
ACACCCTGTG (SEQ ID NO: 496); CACCCTGTGA (SEQ ID NO: 497);
10 ACCCTGTGAG (SEQ ID NO: 498); CCCTGTGAGC (SEQ ID NO: 499);
CCTGTGAGCC (SEQ ID NO: 500); CTGTGAGCCT (SEQ ID NO: 501);
TGTGAGCCTG (SEQ ID NO: 502); GTGAGCCTGC (SEQ ID NO: 503);
TGAGCCTGCA (SEQ ID NO: 504); GAGCCTGCAT (SEQ ID NO: 505);
AGCCTGCATG (SEQ ID NO: 506); GCCTGCATGG (SEQ ID NO: 507);
15 CCTGCATGGA (SEQ ID NO: 508); CTGCATGGAA (SEQ ID NO: 509);
TGCATGGAAT (SEQ ID NO: 510); GCATGGAATG (SEQ ID NO: 511);
CATGGAATGG (SEQ ID NO: 512); ATGGAATGGA (SEQ ID NO: 513);
TGAATGGAT (SEQ ID NO: 514); GGAATGGATG (SEQ ID NO: 515);
GAATGGATGA (SEQ ID NO: 516); AATGGATGAC (SEQ ID NO: 517);
20 ATGGATGACC (SEQ ID NO: 518); TGGATGACCC (SEQ ID NO: 519);
GGATGACCCT (SEQ ID NO: 520); GATGACCCTG (SEQ ID NO: 521);
ATGACCCTGA (SEQ ID NO: 522); TGACCCTGAG (SEQ ID NO: 523);
GACCCTGAGA (SEQ ID NO: 524); ACCCTGAGAG (SEQ ID NO: 525);
CCCTGAGAGA (SEQ ID NO: 526); CCTGAGAGAG (SEQ ID NO: 527);
25 CTGAGAGAGA (SEQ ID NO: 528); TGAGAGAGAA (SEQ ID NO: 529);
GAGAGAGAAG (SEQ ID NO: 530); AGAGAGAAGT (SEQ ID NO: 531);
GAGAGAAGTG (SEQ ID NO: 532); AGAGAAGTGT (SEQ ID NO: 533);
GAGAAGTGTT (SEQ ID NO: 534); AGAAGTGTTA (SEQ ID NO: 535);
GAAGTGTTAG (SEQ ID NO: 536); AAGTGTTAGA (SEQ ID NO: 537);
30 AGTGTTAGAG (SEQ ID NO: 538); GTGTTAGAGT (SEQ ID NO: 539);
TGTTAGAGTG (SEQ ID NO: 540); GTTAGAGTGG (SEQ ID NO: 541);
TTAGAGTGGA (SEQ ID NO: 542); TAGAGTGAG (SEQ ID NO: 543);
AGAGTGAGG (SEQ ID NO: 544); GAGTGAGGT (SEQ ID NO: 545);
AGTGAGGTT (SEQ ID NO: 546); GTGAGGTTT (SEQ ID NO: 547);
35 TGGAGGTTTG (SEQ ID NO: 548); GGAGGTTTGA (SEQ ID NO: 549);
GAGGTTTGAC (SEQ ID NO: 550); AGGTTTGACA (SEQ ID NO: 551);
GGTTTGACAG (SEQ ID NO: 552); GTTTGACAGC (SEQ ID NO: 553);
TTTGACAGCC (SEQ ID NO: 554); TTGACAGCCG (SEQ ID NO: 555);

30

35

- wherein said deletion encompasses one or more decanucleotides from the *nef* gene of HIV-1_{NI43} or corresponding sequences from another pathogenic strain of HIV-1

defined in (or substantially analogous to) SEQ ID NOs:803 to 841:

	ACCAGCTTGT [SEQ ID NO:803]	CCAGCTTGTT [SEQ ID NO:804]
	CAGCTTGTTA [SEQ ID NO:805]	AGCTTGTTAC [SEQ ID NO:806]
	GCTTGTTACA [SEQ ID NO:807]	CTTGTTACAC [SEQ ID NO:808]
5	TTGTTACACC [SEQ ID NO:809]	TGTTACACCC [SEQ ID NO:810]
	GTTACACCCT [SEQ ID NO:811]	TTACACCCTG [SEQ ID NO:812]
	TACACCCTGT [SEQ ID NO:813]	ACACCCTGTG [SEQ ID NO:814]
	CACCCTGTGA [SEQ ID NO:815]	ACCCTGTGAG [SEQ ID NO:816]
	CCCTGTGAGC [SEQ ID NO:817]	CCTGTGAGCC [SEQ ID NO:818]
10	CTGTGAGCCT [SEQ ID NO:819]	TGTGAGCCTG [SEQ ID NO:820]
	GTGAGCCTGC [SEQ ID NO:821]	TGAGCCTGCA [SEQ ID NO:822]
	GAGCCTGCAT [SEQ ID NO:823]	AGCCTGCATG [SEQ ID NO:824]
	GCCTGCATGG [SEQ ID NO:825]	CCTGCATGGA [SEQ ID NO:826]
	CTGCATGGAA [SEQ ID NO:827]	TGCATGGAAT [SEQ ID NO:828]
15	GCATGGAATG [SEQ ID NO:829]	CATGGAATGG [SEQ ID NO:830]
	ATOGAATGGA [SEQ ID NO:831]	TGGAATGGAT [SEQ ID NO:832]
	GGAATGGATG [SEQ ID NO:833]	GAATGGATGA [SEQ ID NO:834]
	AATGGATGAC [SEQ ID NO:835]	ATGGATGACC [SEQ ID NO:836]
	TGGATGACCC [SEQ ID NO:837]	GGATGACCCT [SEQ ID NO:838]
20	GATGACCCTG [SEQ ID NO:839]	ATGACCCTGA [SEQ ID NO:840]
	TGACCCTGAG [SEQ ID NO:841]	

Generally, the subject HIV-1 isolate is non-pathogenic as hereinbefore defined.

Additionally, reference herein to "a deletion" includes reference to a contiguous or non-

contiguous series of two or more deletions.

The non-pathogenic isolate may carry a single decanucleotide deletion or may carry more than one decanucleotide deletion. Where it carries multiple deletions these may all correspond to a contiguous sequence or be from different parts of the *nef* gene.

Furthermore, the terminal end portions of a deletion may lie within a decanucleotide as defined above. It is emphasised that the present invention extends to analogous sequences from other pathogenic strains of HIV-1 which might carry *nef* genes with a slightly altered sequence relative to HIV-1_{NL43}.

In a most preferred embodiment of the present invention, there is provided a non-pathogenic strain of HIV-1 carrying a nucleotide sequence in its genome as set forth in SEQ ID No. 614:

5 GAAGAGATTTGGGAGAACATGACCTGGATGCAGTGGGAAAAAGAAATTCACAATCACAC
AAAATACATATACTCCTTACTTGAAAAATCGCAGAACCAACAAGAAAAGAATGAACAAG
AACTATTGGAATTGGATCAATGGGCAAGTTTGTGGAATTGGTTTGACATAACAAAATGG
CTGTGGTATATAAAAATATTTCATAATGGTAGTAGGAGGCTTGATAGGTTTAAGAATAGT
TTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCGTTTC
10 AGACCCTCCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGAAGGT
GGAGAGAGAGACAGAGACAGATCCACTCGATTAGTACACGGATTCTTAGCACTTTTCTG
GGACGACCTGAGGAGCCTGTGCCTCTTCCTCTACCACCACTTGAGAGACTTACTCTTGA
TTGTAACAAGGATTGTGGAACCTTCTGGGACCGAGGGGATGGGAAGCCCTCAAATATTGG
TGGAACCTCCTAAAGTATTGGAGCCAGGAACGCGAGAAGAGTGCTGTTATCTTGCTCAA
15 TGCCACCGCCATAGCAGTAGCTGAGGGGACAGATAGAGTTTTAGAAGTATTACAAAGAG
CTTATAGAGCTATCCTCCACATACCTAGAAGAATAAGACAGGGCCTCGAAATGGCTTTG
CTATAAAATGGGTGGCAAGTGAGCAAAAAGTAGTGTAGTCAGATAGCATGCATCATAAG
GGGTGGGGGCCAACAACTAACAAATGCTGATCGTGCTGGCTAGAAGCACAAGAGAAGGA
AGAAGCGGGTTTTCCAGTCAAACCTCAGGTAGCTGTAGATCTTAGCCACTTTTTTAAAG
20 AAAAGGGGGGAGCTGGAAGGGCTAATTCACTCCCAAGAAGACAAGATACACAGTGCTGC
AACTATTACCAGTGGAGTCAGCGAAGATAGAAGAGGCCAATGGAGGAGAAAACACAG
ATTGTTCTGTTGGGGACTTTCCATCGTTGGGGACTTTCCAAGGCGCGGTGGCCTGGGT
GACTAGTTCGGGTGGGGACTTTCCAAGAAGGCGCGGCTGGGCGGGACTGGGGAGTGGC
GAGCCCTCAGATGCTGCATATAAGCAGCTGCTTTCTGCTGTTACTGGGTCTCTCGGGTT
25 AGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTC
AATAAGCTTGCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGT
ATCTAGA;

and/or SEQ ID NO: 615:

30 GAAACAATTTGGGATAACATGACCTGGATGCAGTGGGAAAGAGAAATTGACAATTACAC
AAACATAATATACACCTTAATTGAAGAATCGCAGAACCAACAAGAAAAAATGAACTAG
AATTATTGGAATTGGATAAATGGGCAATTTGTGGAATTGGTTTAGTATATCAAACCTGG
CTATGGTATATAAAATATTTCATAATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGT
TTTTACTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCGTTTC
35 AGACCCACCTCCCAACCCCGAAGGGACCCGACAGGCCAGAAGGAATCGAAGAAGAAGGT
GGAGAGAGAGACAGAAGCAGCTCCACTCGATTAGTGCACGGATTCTTAGCACTTTTCTG
GGACGACCTGAGGAGTCTGTGCCTCTTCAGCTACCACCACTTGAGAGACTTACTCTTGA

- 41 -

TTGTAACGAGGATTGTGGAACCTCTGGGACGCAGGGGATGGGAAGCCCTCAAATACTGG
 TGGAAATCTCCTGCAGTATTGGAGGCAGGAACTACAGAAGAGTGCTGTTAGCTTGTTC
 TGGCACGGCCATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGCTTTACGAAGGG
 CTTATAGAGCTATTCTCCACATACCTAGAAGAATAAGACAGGGCTTAGAAAGGGCTTTG
 5 CTATAAAATGGGTGGCAAGTGGTCAGAAAGTAGTGTGGTTAGAAGGCATGTACCTTTAA
 GACAAGGCAGCTATAGATCTTAGCCGCTTTTAAAAGAAAAGGGGGGACTGGAAGGGCT
 AATTCACCTCACAGAGAAGATCAGTTGAACCAGAAGAAGATAGAAGAGGCCATGAAGAAG
 AAAACAACAGATTGTTCCGTTTGTTCGTTGGGGACTTTCCAGGAGACGTGGCCTGAGT
 GATAAGCCGCTGGGGACTTTCCGAAGAGGCGTGACGGGACTTTCCAAGGCGACGTGGCC
 10 TGGGCGGGACTGGGGAGTGGCGAGCCCTCAGATGCTGCATATAAGCAGCTGCTTTCTGC
 CTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAG
 GGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCCTTGAGTGCTTCAAGTAGTGTGTGCC
 CGTCTGTTGTGTGACTCTGGTATCTAGA.

- 15 The present invention, however, extends to HIV-1 isolates which are non-pathogenic; carry genomes capable of hybridising under low stringency conditions to SEQ ID NO: 614 or SEQ ID NO: 615; and which do not direct the synthesis of a full length *nef* gene product.
- 20 In a further embodiment the present invention contemplates a viral isolate which:
- (i) is reactive to antibodies to a glycoprotein from HIV-1 such as at least one of gp41-45, gp120 and/or gp160;
 - (ii) carries a genome or a part or fragment thereof capable of hybridising under medium stringency conditions to a nucleotide sequence as set forth in SEQ ID
 - 25 NO: 1 or a complementary form thereof or an analogous sequence from another pathogenic strain of HIV-1;
 - (iii) carries a deletion of at least ten nucleotides in a region corresponding to the LTR region in HIV-1_{NL43}; and
- wherein said deletion encompasses one or more of the following decanucleotides from
- 30 the LTR region of HIV-1_{NL43} or corresponding sequences from another pathogenic strain of HIV-1:

GCTTTTTGCC (SEQ ID NO: 652); CTTTTTGCCT (SEQ ID NO: 653);
 TTTTTGCCTG (SEQ ID NO: 654); TTTTGCCTGT (SEQ ID NO: 655);
 35 TTTGCCTGTA (SEQ ID NO: 656); TTGCCTGTAC (SEQ ID NO: 657);

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TGCCTGTACT (SEQ ID NO: 658); GCCTGTACTG (SEQ ID NO: 659);
 CCTGTACTGG (SEQ ID NO: 660); CTGTACTGGG (SEQ ID NO: 661);
 TGTACTGGGT (SEQ ID NO: 662); GTACTGGGTC (SEQ ID NO: 663);
 TACTGGGTCT (SEQ ID NO: 664); ACTGGGTCTC (SEQ ID NO: 665);
 5 CTGGGTCTCT (SEQ ID NO: 666); TGGGTCTCTC (SEQ ID NO: 667);
 GGGTCTCTCT (SEQ ID NO: 668); GGTCTCTCTG (SEQ ID NO: 669);
 GTCTCTCTGG (SEQ ID NO: 670); TCTCTCTGGT (SEQ ID NO: 671);
 CTCTCTGGTT (SEQ ID NO: 672); TCTCTGGTTA (SEQ ID NO: 673);
 CTCTGGTTAG (SEQ ID NO: 674); TCTCTGGTTA (SEQ ID NO: 675);
 10 CTGGTTAGAC (SEQ ID NO: 676); TGGTTAGACC (SEQ ID NO: 677);
 GGTAGACCA (SEQ ID NO: 678); GTTAGACCAG (SEQ ID NO: 679);
 TTAGACCAGA (SEQ ID NO: 680); TAGACCAGAT (SEQ ID NO: 681);
 AGACCAGATC (SEQ ID NO: 682); GACCAGATCT (SEQ ID NO: 683);
 ACCAGATCTG (SEQ ID NO: 684); CCAGATCTGA (SEQ ID NO: 685);
 15 CAGATCTGAG (SEQ ID NO: 686); AGATCTGAGC (SEQ ID NO: 687);
 GATCTGAGCC (SEQ ID NO: 688); ATCTGAGCCT (SEQ ID NO: 689);
 TCTGAGCCTG (SEQ ID NO: 690); CTGAGCCTGG (SEQ ID NO: 691);
 TGAGCCTGGG (SEQ ID NO: 692); GAGCCTGGGA (SEQ ID NO: 693);
 AGCCTGGGAG (SEQ ID NO: 694); GCCTGGGAGC (SEQ ID NO: 695);
 20 CCTGGGAGCT (SEQ ID NO: 696); CTGGGAGCTC (SEQ ID NO: 697);
 TGGGAGCTCT (SEQ ID NO: 698); GGGAGCTCTC (SEQ ID NO: 699);
 GGAGCTCTCT (SEQ ID NO: 700); GAGCTCTCTG (SEQ ID NO: 701);
 AGCTCTCTGG (SEQ ID NO: 702); GCTCTCTGGC (SEQ ID NO: 703);
 CTCTCTGGCT (SEQ ID NO: 704); TCTCTGGCTA (SEQ ID NO: 705);
 25 CTCTGGCTAA (SEQ ID NO: 706); TCTGGCTAAC (SEQ ID NO: 707);
 CTGGCTAACT (SEQ ID NO: 708); TGGCTAACTA (SEQ ID NO: 709);
 GGCTAACTAG (SEQ ID NO: 710); GCTAACTAGG (SEQ ID NO: 711);
 CTAAGTAGGG (SEQ ID NO: 712); TAACTAGGGA (SEQ ID NO: 713);
 AACTAGGGAA (SEQ ID NO: 714); ACTAGGGAAC (SEQ ID NO: 715);
 30 CTAGGGGAACC (SEQ ID NO: 716); TAGGGGAACCC (SEQ ID NO: 717);
 AGGGGAACCCA (SEQ ID NO: 718); GGGAACCCAC (SEQ ID NO: 719);
 GGAACCCACT (SEQ ID NO: 720); GAACCCACTG (SEQ ID NO: 721);
 AACCCACTGC (SEQ ID NO: 722); ACCCACTGCT (SEQ ID NO: 723);
 CCCACTGCTT (SEQ ID NO: 724); CCACTGCTTA (SEQ ID NO: 725);
 35 CACTGCTTAA (SEQ ID NO: 726); ACTGCTTAAG (SEQ ID NO: 727);
 CTGCTTAAGC (SEQ ID NO: 728); TGCTTAAGCC (SEQ ID NO: 729);
 GCTTAAGCCT (SEQ ID NO: 730); CTTAAGCCTC (SEQ ID NO: 731);
 TTAAGCCTCA (SEQ ID NO: 732); TAAGCCTCAA (SEQ ID NO: 733);

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 00445-0329160

AAGCCTCAAT (SEQ ID NO: 734); AGCCTCAATA (SEQ ID NO: 735);
 GCCTCAATAA (SEQ ID NO: 736); CCTCAATAAA (SEQ ID NO: 737);
 CTCAATAAAG (SEQ ID NO: 738); TCAATAAAGC (SEQ ID NO: 739);
 CAATAAAGCT (SEQ ID NO: 740); AATAAAGCTT (SEQ ID NO: 741);
 5 ATAAAGCTTG (SEQ ID NO: 742); TAAAGCTTGC (SEQ ID NO: 743);
 AAAGCTTGCC (SEQ ID NO: 744); AAGCTTGCCT (SEQ ID NO: 745);
 AGCTTGCCCT (SEQ ID NO: 746); GCTTGCCCTG (SEQ ID NO: 747);
 CTTGCCTTGA (SEQ ID NO: 748); TTGCCTTGAG (SEQ ID NO: 749);
 TGCCTTGAGT (SEQ ID NO: 750); GCCTTGAGTG (SEQ ID NO: 751);
 10 CCTTGAGTGC (SEQ ID NO: 752); CTTGAGTGCT (SEQ ID NO: 753);
 TTGAGTGCTT (SEQ ID NO: 754); TGAGTGCTTC (SEQ ID NO: 755);
 GAGTGCTTCA (SEQ ID NO: 756); AGTGCTTCAA (SEQ ID NO: 757);
 GTGCTTCAAG (SEQ ID NO: 758); TGCTTCAAGT (SEQ ID NO: 759);
 GCTTCAAGTA (SEQ ID NO: 760); CTTCAAGTAG (SEQ ID NO: 761);
 15 TTCAAGTAGT (SEQ ID NO: 762); TCAAGTAGTG (SEQ ID NO: 763);
 CAAGTAGTGT (SEQ ID NO: 764); AAGTAGTGTG (SEQ ID NO: 765);
 AGTAGTGTGT (SEQ ID NO: 766); GTAGTGTGTG (SEQ ID NO: 767);
 TAGTGTGTGC (SEQ ID NO: 768); AGTGTGTGCC (SEQ ID NO: 769);
 GTGTGTGCCC (SEQ ID NO: 770); TGTGTGCCCC (SEQ ID NO: 771);
 20 GTGTGCCCCG (SEQ ID NO: 772); TGTGCCCCGC (SEQ ID NO: 773);
 GTGCCCCGTCT (SEQ ID NO: 774); TGCCCCGTCTG (SEQ ID NO: 775);
 GCCCGTCTGT (SEQ ID NO: 776); CCCGTCTGTT (SEQ ID NO: 777);
 CCGTCTGTTG (SEQ ID NO: 778); CGTCTGTTGT (SEQ ID NO: 779);
 GTCTGTTGTG (SEQ ID NO: 780); TCTGTTGTGT (SEQ ID NO: 781);
 25 CTGTTGTGTG (SEQ ID NO: 782); TGTGTTGTGA (SEQ ID NO: 783);
 GTTGTGTGAC (SEQ ID NO: 784); TTGTGTGACT (SEQ ID NO: 785);
 TGTGTGACTC (SEQ ID NO: 786); GTGTGACTCT (SEQ ID NO: 787);
 TGTGTGACTC (SEQ ID NO: 788); GTGTGACTCT (SEQ ID NO: 789);
 TGTGACTCTG (SEQ ID NO: 790); GTGACTCTGG (SEQ ID NO: 791);
 30 TGACTCTGGT (SEQ ID NO: 792); GACTCTGGTA (SEQ ID NO: 793);
 ACTCTGGTAA (SEQ ID NO: 794); CTCTGGTAAC (SEQ ID NO: 795);
 TCTGGTAACT (SEQ ID NO: 796); CTGGTAACTA (SEQ ID NO: 797);
 TGGTAACTAG (SEQ ID NO: 798); GGTAAC TAGA (SEQ ID NO: 799).

- 35 The non-pathogenic isolate may carry a single decanucleotide deletion in the LTR region
 or may carry multiple deletions in the same region or in the LTR region and another
 region such as the *nef* gene. In particular, the mutation may be in the LTR/*nef* overlap

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- 44 -

region. Where it carries multiple deletions, these may correspond to a contiguous sequence or be from different parts of the LTR region and/or *nef* gene. Furthermore, the terminal end portions of a deletion may lie within a decanucleotide as defined above.

- 5 Yet another aspect of the present invention provides an infectious molecular clone comprising genetic sequences derived from the non-pathogenic HIV-1 isolates as hereinbefore described and includes genetic sequences encoding major structural proteins such as *gag*, *env* and *pol*. Infectious molecular clones are particularly useful as genetic compositions capable of "infecting" host cells without need of viral coat. The infectious
10 molecular clones of the present invention may also be derived from pathogenic HIV-1 strains rendered non-pathogenic as hereindescribed.

- According to this latter embodiment, there is contemplated a method of attenuating a pathogenic strain of HIV-1, said method comprising inducing a mutation in the *nef* gene
15 and/or an LTR region to generate a non-pathogenic HIV-1 strain as hereinbefore described. Preferred mutations are deletions of at least ten nucleotides such as one or more of the decanucleotides as hereinbefore described. Particularly preferred mutations result in modified Nef protein carrying a deletion substantially corresponding to amino acids 162 to 177 of Nef from wild-type HIV-1. The mutations may also constitute
20 substitutions and/or insertions of heterologous nucleic acid molecules in the *nef* and/or LTR regions such as the incorporation of a sense (i.e. co-suppression) or antisense molecule.

- In still yet another embodiment of the present invention, there is provided an isolated,
25 non-pathogenic strain of HIV-1 comprising a deletion in its genome of at least 10 nucleotide within the region of nucleotide 8787 and 9709 and more particularly within the region 8800 and 9700 and even more preferably within the region 8800 and 9410, using the nucleotide numbering of HIV-1_{NL43}.

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In one embodiment, the deletion of at least 10 nucleotides is from within a region selected from the list consisting of (using the nucleotide numbers of HIV-1_{NL43}):

- | | | | |
|---|------------|-------|----------------|
| 5 | nucleotide | (i) | 8830-8862; |
| | | (ii) | 9009-9035; |
| | | (iii) | 9019-9029; and |
| | | (iv) | 9033-9049. |

In another embodiment, the deletion of at least 10 nucleotides is from within a region
10 selected from the list consisting of (using the nucleotide numbers of HIV-1_{NL43}):

- | | | |
|------------|--------|----------------|
| nucleotide | (v) | 9281-9371; |
| | (vi) | 9281-9362; |
| | (vii) | 9105-9224; and |
| | (viii) | 9271-9370. |

15

In yet another embodiment, the deletion of at least 10 nucleotides is from within a region selected from the list consisting of (using the nucleotide numbers of HIV-1_{NL43}):

- | | | | |
|----|------------|-------|----------------|
| | nucleotide | (ix) | 8882-8928; |
| | | (x) | 8850-9006; |
| 20 | | (xi) | 8792-9041; and |
| | | (xii) | 9112-9204. |

In still yet another embodiment, the deletion of at least 10 nucleotides is from within a region selected from the list consisting of (using the nucleotide numbers of HIV-1_{NL43}):

- 25 nucleotide (xiii) 9105-9224;
(xiv) 9389-9395; and
(xv) 9281-9366.

The above embodiments including any combinations thereof or functional equivalents thereof. Most preferred variants of HIV-1 are defined in Table 3.

Reference herein to the non-pathogenic HIV-1 strains of the present invention includes reference to components, parts, fragments and derivatives thereof including both genetic and non-genetic material. Furthermore, the non-pathogenic HIV-1 strains may be in
5 isolated form or resident in peripheral blood mononuclear cells (PBMCs) or other like cells where the genome of the HIV-1 strains is integrated as DNA from said HIV-1 strains such as proviral DNA. In addition, the present invention extends to recombinant virus such as from (or resident in) prokaryotes or eukaryotes as well as in the form of infectious molecular clones.

10

Accordingly, the present invention provides for the non-pathogenic HIV-1 isolate, genomic material therefrom, complementary proviral DNA, molecular infectious clones, recombinant viral particles or genetic sequences therefrom or cells expressing same or blood cells carrying proviral DNA or to any mutants, derivatives, components,
15 fragments, parts, homologues or analogues of the foregoing.

Another aspect of the present invention contemplates a synthetic peptide comprising a sequence of amino acids as defined in SEQ ID NO:699 or a part or a fragment thereof. The synthetic peptide generally comprises at least four, preferably at least five, more
20 preferably at least six and even more preferably at least seven or more of the amino acids as defined in SEQ ID NO:699. Furthermore, the synthetic peptides may comprise chemically modified amino acids or structurally, functionally and/or stereochemically equivalent substitute amino acids. Such synthetic peptides are useful in diagnostic protocols or in therapeutic regimens, such as in generating antibodies to that particular
25 region of the Nef protein. By administering the synthetic peptides of this aspect of the present invention, higher titres of antibodies to a particular region of Nef may be obtained compared to what would be stimulated if a larger portion of Nef is used.

The non-pathogenic HIV-1 strains of the present invention are particularly useful in the
30 development of therapeutic compositions, therapeutic molecules and/or diagnostic reagents. With regards to the former, the non-pathogenic HIV-1 strain may be considered as a live attenuated vaccine where individuals carrying DNA derived from

- 47 -

said non-pathogenic HIV-1 strain such as proviral DNA in target cells are protected from infection by a corresponding pathogenic strain. The term "vaccine" is used in its broadest sense as a therapeutic composition or molecule which prevents or reduces HIV-1 infection or risk of infection or which ameliorates the symptoms of infection. It may
5 involve the stimulation of an immune response or may involve blocking HIV-1 cells receptors and/or the use of genetic compositions, for example, to introduce ribozymes or antisense molecules to HIV-1 directed genetic sequences or to prepare infectious molecular clones. For convenience, all such compositions are referred hereinafter to "therapeutic compositions".

10

Accordingly, the present invention contemplates a method for inhibiting or reducing the risk of infection by a pathogenic strain of HIV-1, said method comprising administering to a subject a non-pathogenic HIV-1 as hereinbefore defined in an amount effective to infect target cells and to generate target cells carrying proviral DNA from said non-
15 pathogenic HIV-1. More particularly, the present invention contemplates a method for inhibiting or reducing productive infection of an individual by a pathogenic strain of HIV-1, said method comprising administering to a subject a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate target cells carrying proviral DNA from said non-pathogenic HIV-1. By "productive infection" as used in
20 the specification and claims herein is meant the infection of a cell or cells by a pathogenic strain of HIV-1 which leads ultimately to the symptomology of AIDS or AIDS related diseases. A cell infected productively produces pathogenic virions. By definition, infection of an individual by a non-pathogenic strain of HIV-1 would not lead to productive infection. Non-pathogenic HIV-1 strains generally replicate to a sufficient
25 extent to protect cells against challenge by virulent or pathogenic strains. The methods of the present invention are applicable prophylactically (i.e. to prevent *de novo* infection) or therapeutically (i.e. to reduce or slow disease progression).

The present invention further provides a method for vaccinating an individual against
30 the development of AIDS or AIDS-related diseases, said method comprising administering to said individual a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate target cells carrying proviral DNA from

- 48 -

said non-pathogenic HIV-1. The term "vaccinating" should not be taken as limiting the invention to the prevention of HIV-1 infection by solely immunological means. The term "vaccinating" includes any means of preventing productive infection of an individual by pathogenic HIV-1. Particularly, preferred non-pathogenic strains of HIV-1 according to these aspects of the present invention are generally defined as encoding a modified protein such as a modified Nef protein and in particular a modified Nef protein which is substantially non-interactive to antibodies to amino acids 162 to 177 of wild-type HIV-1 Nef.

- 10 As an alternative to the above methods, a therapeutic composition as hereinbefore defined is administered. The non-pathogenic isolate may be administered *inter alia* as an isolated viral preparation or *via* infected blood cells. Another aspect of the invention provides a therapeutic composition for inhibiting or reducing the risk of infection by a pathogenic strain of HIV-1 said therapeutic composition comprising a non-pathogenic strain of HIV-1 or genetic sequences derived therefrom as hereinbefore described and optionally one or more pharmaceutically acceptable carriers and/or diluents. In a further embodiment, the therapeutic compositions comprise the synthetic peptides comprising an amino acid sequence as set forth in SEQ ID NO:699 or a part, fragment or homologue thereof. Such a vaccine would generate high titre antibodies to a specific region of Nef protein.

- The therapeutic composition of the present invention is generally suitable for intravenous, intraperitoneal, intramuscular, intramucosal (e.g. nasal spray, respiratory spray) or other forms of parenteral administration. The therapeutic composition might also be administered *via* an implant or rectally or orally. In addition to the mutations contemplated above, the non-pathogenic HIV-1 strain may also contain one or more other mutations to further reduce the risk of reversion to virulence and/or to insert a genetic sequence capable of providing directly or indirectly an identifiable signal, having further anti-HIV-1 properties and/or immunostimulatory or cell regulatory properties.

30

For example, the non-pathogenic HIV-1 isolate in the therapeutic composition may comprise additional genetic material capable of directing expression of antisense nucleotide sequences to inhibit expression of one or more proteins encoded by a pathogenic strain of HIV-1. Alternatively, sense co-suppression may be employed. Preferred sense or antisense molecules would reduce expression of the *nef* gene or affect normal functioning of the LTR region. In a particularly preferred embodiment, the nucleotide sequence encoding amino acids 162 to 177 is targetted by sense or antisense molecules.

10

According to this embodiment, the non-pathogenic HIV-1 strain may be considered as a targeting agent to introduce genetic constructs capable of reducing expression of one or more HIV-1 proteins or polypeptides. In this embodiment there is provided a viral isolate which:

- 15 (i) is genetically or immunologically related to a pathogenic strain of HIV-1;
- (ii) is substantially non-pathogenic in human subjects;
- (iii) comprises a first nucleotide sequence constituting its genome which is capable of hybridising under medium stringency conditions to SEQ ID NO: 1 or a complementary form thereof; and
- 20 (iv) comprises a second nucleotide sequence within said first nucleotide sequence and which second nucleotide sequence directs expression of a mRNA molecule capable of inhibiting, reducing or otherwise down-regulating translation of a protein or polypeptide encoded by a pathogenic strain of HIV-1 or inhibit, reduce or otherwise down regulate operation of a non-protein encoding a region of a
- 25 pathogenic strain of HIV-1.

Preferred proteins or polypeptides targeted for reduced expression are those encoded by one or more of the following: *gag*, *pol*, *env*, *tat*, *rev*, *vpu*, *vpr*, *vif* and/or *nef* genes. The most preferred protein or polypeptide targeted for reduced expression is the product of the *nef* gene. Alternatively, the target nucleotide sequence does not encode a polypeptide or protein but is required for other functions such as integration or excision from the human genome or expression of genes on the viral genome. An example of

30

such a nucleotide sequence is the LTR region. Accordingly, the present invention extends to disruption to the function of such regions.

In a particularly preferred embodiment there is provided a viral isolate which:

- 5 (i) is genetically or immunologically related to a pathogenic strain of HIV-1;
- (ii) is substantially non-pathogenic in human subjects; and
- (iii) comprises a nucleotide sequence which directs expression of a mRNA molecule capable of inhibiting, reducing or otherwise down-regulating translation of Nef.

- 10 Preferably, the nucleotide sequence reduces levels of amino acids 162 to 177 in Nef. The above aspect relates to use of antisense technology. The present invention extends, however, to use of ribozymes and/or co-suppression to achieve the same results. In an alternative embodiment, or in addition to, the second (or optionally a third) nucleotide sequence encodes an antiviral agent (e.g. interferon) and/or an immune enhancing agent.

15

- The identification of deletions *inter alia* in the *nef* gene and/or LTR region in asymptomatic subjects provides a unique opportunity to study the *in vivo* effects of attenuated HIV-1 strains carrying one or more mutations in selected genetic regions. In particular, the present invention provides a means for designing therapeutic compositions
- 20 directed to inhibiting expression of a *nef* gene and/or LTR region in a pathogenic HIV-1 strain (such as contemplated above) as well as developing a therapeutic regimen aimed at inhibiting the activity of the *nef* gene product for the function of the LTR region. According to this latter embodiment, the present invention provides a therapeutic composition comprising a molecule capable of inhibiting the intracellular activity of the
 - 25 *nef* gene product and/or LTR region, said composition further comprising one or more pharmaceutically acceptable carriers and/or diluents. In one preferred embodiment, the inhibition effects amino acids 162 to 177 of Nef.

- The molecule contemplated by the above aspect of the subject invention may be a
- 30 protein, polypeptide, peptide, chemical compound, sugar moiety or derivative of the *nef* gene product. The molecule will need to be capable of entering an infected cell. Where the molecule is a protein, polypeptide or peptide, it may be encoded by the second

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- 51 -

nucleotide sequence on the targeting vector as contemplated above. Alternatively, the molecule may be a nucleic acid molecule capable of targeting the *nef* gene or LTR region. Where the *nef* gene is targetted, the preferred region is the nucleotide sequence which encodes amino acids 162 to 177 of Nef.

5

The deletion mutants of the present invention may result in a modified *nef* gene product either having no readily discernable activity or having activity different to the naturally occurring *nef* protein. In any event, if a mutant *nef* gene product is produced, it will generally have a lower molecular weight than the naturally occurring *nef* protein and will
10 have a different overall amino acid sequence. Importantly, it will be immunologically distinguishable from wild-type Nef in that it will be substantially non-interactive with antibodies to a particular region of Nef, such as amino acids 162 to 177 of wild-type Nef. This provides, therefore, for a means for diagnosing individuals with benign HIV-1 infection by, for example, assaying for a modified *nef* protein or screening for a
15 modified *nef* gene sequence. Alternatively, benign HIV-1 infection may be detected by assaying for a modified LTR region such as an altered nucleotide sequence.

These aforementioned aspects of the present invention apply to screening deletion, truncation or other mutants of HIV-1-derived proteins where such mutations result in a
20 strain of HIV-1 being substantially non-pathogenic. Although a variety of procedures are available to detect a modified HIV-1-derived protein, a particularly convenient approach is to screen HIV-1 infected individuals for the absence of antibodies to the deleted or truncated portion of a target protein.

25 According to one embodiment there is provided a method for determining the pathogenicity of a strain of HIV-1 after said HIV-1 strain infects cells of an individual said method comprising contacting a biological sample from said individual with a peptide corresponding to a deleted or truncated region of an HIV-1-derived protein and screening for the absence of antibody binding to said peptide, wherein the absence of
30 antibody binding is indicative of a deletion or truncation in that protein and further indicative of the non-pathogenicity of said strain of HIV-1.

Although this general methodology is applicable to any protein encoded by HIV-1 which is critical for pathogenicity in a host, it is particularly useful in screening deletions in the Nef protein. An exemplary deletion in the Nef protein is all or part of the sequence of amino acids 162 to 177 of Nef. Preferably, the assay would include a positive control such that where antibodies are present to Nef, such antibodies would bind to this positive control. When a Nef protein carries a deletion at or about amino acids 162 to 177, antibodies to this region would be absent in an individual infected by a non-pathogenic strain of HIV-1 and no binding would be detected to a peptide covering this region.

- 10 According to a particularly preferred embodiment, there is contemplated a method for determining the pathogenicity of an HIV-1 strain after said strain infects cells of an individual, said method comprising contacting a biological sample from said individual with an effective amount of a peptide having an amino acid sequence comprising or
- 15 within amino acids 162 to 177 of wild-type HIV-1_{NL43} Nef, said contact being for a time and under conditions sufficient for an antibody if present in said biological sample to form a complex with said peptide and then detecting the presence of said complex wherein the absence of a complex in an individual seropositive for HIV-1 is indicative of that the individual being infected with a non-pathogenic strain of HIV-1. The method
- 20 may also comprise contacting the biological sample with one or more peptides derived from other regions of Nef such as flanking regions to amino acids 162 to 177 where antibodies to such other regions may be expected even in non-pathogenic HIV-1 strains. This would provide a suitable positive control. A biological sample according to this embodiment would be any source of antibodies such as serum and whole blood.
- 25 Preferably, the peptides are immobilized to a solid support as described below. This method of the present invention is also applicable for determining the risk of an individual seropositive for HIV-1 developing symptoms of AIDS. Again, substantial absence of antibodies to amino acids 162 to 177 of Nef in an HIV-1 seropositive individual would be indicative of a low risk of an individual developing AIDS.

Other methods of screening for the pathogenicity or otherwise of strains of HIV-1 readily become apparent as a result of the present invention. For example, antibodies may be first generated to modified Nef proteins from non-pathogenic strains of HIV-1
5 where such antibodies would not recognise wild-type Nef protein.

According to one embodiment, there is provided a method for determining the pathogenicity of an HIV-1 strain after said HIV-1 strain infects cells of an individual, said method comprising contacting a biological sample from said individual with an
10 effective amount of an antibody specific to a *nef* protein from a non-pathogenic strain of HIV-1 (as hereinbefore defined) for a time and under conditions sufficient to form an antibody-modified *nef* protein complex and then detecting said complex. The presence of said complex is indicative of a modified *nef* gene product and of the non-pathogenicity of the strain of HIV-1. Alternatively, the isolated Nef could be tested
15 against a panel of antibodies where certain antibodies are specific to a deleted region. The absence of antibody binding would be indicative of a deletion and, therefore, a modified Nef protein and in turn a putative non-pathogenic form of the virus. The biological sample is a sample likely to contain the modified *nef* gene product such as tissue extract or cell extract of an infected cell. However, where the modified *nef* gene
20 product is capable of permeation or transport out of the cell, suitable biological fluid would include serum, whole blood, lymph and mucosal secretion amongst other fluids.

Many variations in the aforementioned assays are possible and are contemplated herein. For example, an assay could also be based on the inability for a *nef* specific antibody
25 to bind to a modified *nef* protein. For the purposes of the present invention the term "contacting" including "mixing".

The presence of a modified *nef* molecule, such as a molecule carrying a deletion, or other suitable HIV-1 derived protein in biological fluid can be detected using a wide
30 range of immunoassay techniques such as those described in US Patent Nos. 4,016,043, 4,424,279 and 4,018,653. These include both single-site and two-site, or "sandwich", assays of the non-competitive types, as well as in the traditional competitive binding

assays and include ELISA and RIA techniques. Sandwich assays are among the most useful and commonly used assays and are favoured for use in the present invention. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, and by way of example only, in a
5 typical forward assay, a modified *nef* product-specific antibody is immobilised onto a solid substrate to form a first complex and the sample to be tested for modified *nef* product brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-modified *nef* product secondary complex, a second modified *nef* protein antibody, labelled with
10 a reporter molecule capable of producing a detectable signal, is then added and incubated, allowing time sufficient for the formation of a tertiary complex of antibody-modified *nef* product-antibody. Any unreacted material is washed away, and the presence of the tertiary complex is determined by observation of a signal produced by the reporter molecule. The results may either be qualitative, by simple observation of
15 the visible signal or may be quantitated by comparison with a control sample containing known amounts of hapten. Variations of the forward assay include a simultaneous assay, in which both sample and labelled antibody are added simultaneously to the bound antibody, or a reverse assay in which the labelled antibody and sample to be tested are first combined, incubated and then added simultaneously to the bound antibody. These
20 techniques are well known to those skilled in the art, and the possibility of minor variations will be readily apparent. The antibodies used above may be monoclonal or polyclonal. In a preferred embodiment, antibodies to Nef in an individual's biological fluid are screened for using peptides derived from Nef. The absence of antibodies to specific regions of Nef such as amino acids 162 to 177 would be indicative of a non-pathogenic strain of HIV-1. All such assays and variations of such assays are
25 encompassed by the present invention.

The solid substrate is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.
30 The solid supports may be in the form of tubes, beads, discs or microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically

- 55 -

adsorbing the molecule to the insoluble carrier.

By "reporter molecule", as used in the present specification, is meant a molecule which, by its chemical nature, produces an analytically identifiable signal which allows the
5 detection of antigen-bound antibody. Detection may be either qualitative or quantitative. The most commonly used reporter molecules in this type of assay are enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes). In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognised, however, a wide
10 variety of different conjugation techniques exist which are readily available to one skilled in the art. Commonly used enzymes include horseradish peroxidase, glucose oxidase, β -galactosidase and alkaline phosphatase, amongst others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable colour change. It is also possible to
15 employ fluorogenic substrates, which yield a fluorescent product.

Alternatively, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength, the fluorochrome-labelled antibody
20 adsorbs the light energy, inducing a state of excitability in the molecule, followed by emission of the light at a characteristic colour visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining complex is then exposed to the light of the appropriate wavelength, the fluorescence
25 observed indicates the presence of the hapten of interest. Immunofluorescence and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed. It will be readily apparent to the skilled technician how to vary the procedure to suit the required
30 purpose. It will also be apparent that the foregoing can be used to label a modified *nef* product and to use same directly in the detection of, for example, circulatory antibodies specific to said modified *nef* product.

- 56 -

Alternatively, genetic assays may be conducted to screen for aberrations in the *nef* gene and/or LTR region. Such a genetic assay may be by Southern or Northern blot analysis, PCR analysis or the like using oligonucleotides specific to a deleted region of a *nef* gene and/or LTR region.

5

According to this embodiment there is provided a method for determining the pathogenicity of an HIV-1 strain after said HIV-1 strain infects cells of an individual, said method comprising determining directly or indirectly the presence of a deletion mutation in the genome of said HIV-1 wherein the presence of a such a mutation is
 10 indicative of the presence of a non-pathogenic strain of HIV-1. The deletion mutation may result in the genome being unable to synthesize a polypeptide or protein from a pathogenic strain of HIV-1 or may direct the synthesis of a truncated or deleted form of said polypeptide or protein. For example, a Nef protein with amino acids 162 to 177 deleted therefrom. The mutation may also lead to altered expression of a polypeptide
 15 detectable by, for example, decreased synthesis of a particular protein, such as the *nef* gene product. Alternatively, the deletion mutation affects the LTR region or a regulatory region of the HIV-1 genome. In either case, affected viruses may also be detected by, for example, observing low viral copy numbers such as low viral loads.

20 Preferably, said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43}.

Preferably, said non-pathogenic HIV-1 carries a deletion in its genome of at least 10
 25 nucleotides from within a region selected from the list consisting of:

- | | | |
|------------|-------|----------------|
| nucleotide | (i) | 8830-8862; |
| | (ii) | 9009-9035; |
| | (iii) | 9019-9029; and |
| | (iv) | 9033-9049. |

30

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Preferably, said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

- | | | | |
|---|------------|--------|----------------|
| | nucleotide | (v) | 9281-9371; |
| 5 | | (vi) | 9281-9362; |
| | | (vii) | 9105-9224; and |
| | | (viii) | 9271-9370. |

Preferably, said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

- | | | | |
|--|------------|-------|----------------|
| | nucleotide | (ix) | 8882-8928; |
| | | (x) | 8850-9006; |
| | | (xi) | 8792-9041; and |
| | | (xii) | 9112-9204. |

15

Preferably, said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

- | | | | |
|----|------------|--------|----------------|
| | nucleotide | (xiii) | 9105-9224; |
| | | (xiv) | 9389-9395; and |
| 20 | | (xv) | 9281-9366. |

The above nucleotide numbers are based on the nucleotide numbering in the NL43 genome.

25 Particularly preferred oligonucleotides are based on the deleted regions of the *nef* gene and/or LTR region such as but not limited to one or more oligonucleotides based on SEQ ID NO: 2 to SEQ ID NO: 613 and/or SEQ ID NO: 652 to SEQ ID NO: 799.

30 Most preferred deletions include deletions of one or more of SEQ ID NO:803 to 841 which cover amino acids 162 to 177 of Nef. A particularly preferred genetic assay screens for this deletion.

- 58 -

The present invention further extends to kits for the diagnosis of infection by pathogenic strains of HIV-1 or for determining the pathogenicity of infecting virus. The kits would be in compartmental form each comprising one or more suitable reagents for conducting the assay.

5

The present invention is further described by the following non-limiting Examples.

EXAMPLE 1

Source Material

- 10 For the purposes of the following examples, non-pathogenic HIV-1 strains were isolated from recipients of HIV-1 infected blood. The recipients are designated "C18", "C54", "C98", "C49", "C64" and "C124". The donor is identified herein as "D36". The place of isolation may be indicated after the abbreviation of "HIV". For example, St Vincents Hospital, Sydney (HIV_{SV}) or Macfarlane Burnet Centre of Medical Research,
15 Melbourne (HIV_{MBC}).

- Exemplary viral isolates referred to herein as "C18" and "C98" were deposited at the PHLS Centre for Applied Microbiology and Research, European Collection of Animal Cell Cultures (ECACC), Division of Biologics, Porton Down, Salisbury, Wiltshire SP4
20 OJG. C18 was deposited on 17 October, 1994 under Provisional Accession Number V94101706 and C98 was deposited on 31 October, 1994 under Provisional Accession Number V941031169. Another isolate "C54" was deposited at ECACC on 10 March, 1995 under Provisional Accession Number V95031022.

- 25 Figure 11 is a summary of the deletion mutants of the present invention.

Viruses are isolatable by the following procedures:

1. Infected peripheral blood mononuclear cells (PBMCs) were co-cultured with HIV-1 seronegative donor PBMCs. A convenient source of seronegative donor
30 PBMCs is a blood bank. The supernatants and cells are harvested every 7 days and fresh medium added with CD8 depleted PBMCs. CD8 depletion promotes the ability to isolate HIV-1. The culture and procedure is continued for up to

- 59 -

approximately 5 weeks;

2. The infected PBMCs are purified from whole blood and these cells are cultured alone for up to 5 weeks. PMBCs alone are used because the virus is more likely to be monocytotropic. Fresh medium is added weekly and supernatant fluid is harvested at this time;
 3. Supernatant fluids are harvested every approximately 7 days, fresh medium and fresh HIV-1 seronegative CD8 depleted PBMCs are added at this time;
 4. HIV-1 seronegative PBMCs are pretreated with with M-CSF for approximately 72 hours prior to the addition of infected PBMCs. M-CSF has been shown to enhance HIV-1 replication in monocytes (Gendelman *et al*, 1988); and
 5. The supernatant fluid is harvested from the cultures of step 4 every approximately 7 days, fresh medium added together with HIV-1 seronegative stimulated CD8 depleted PBMCs. The virus is isolated from the infected PBMCs.
- A particularly preferred method of isolation is as follows:
- HIV negative donor PBMC were stimulated by culture in RPMI 1640 containing 10% v/v fetal calf serum (FCS), 15 mM N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid, 0.1% w/v sodium bicarbonate with 100 IU/ml penicillin and 100 µg/ml streptomycin with the addition of 10 µg/ml PHA (Wellcome, Temple Hill, Dartford, England) for 72 h prior to co-culture. Fresh patient cells (10×10^6 cells) were then co-cultured with the PHA-activated donor PBMC (10×10^6 cells). Immediately on co-culture 2×10^6 of the mixed cell population were UV irradiated (254nm, $300 \mu\text{W}/\text{cm}^2$, 15sec), added back to the remaining cells and cultured for 29 days. After UV treatment cells were resuspended at 1×10^6 cells/ml in RPMI 1640 containing 10% v/v FCS, 15 mM HEPES, 0.1% w/v sodium bicarbonate, 25 µg/ml glutamine, 100 IU/ml penicillin, 100 µg/ml streptomycin, 2 µg/ml polybrene; 4µg/ml hydrocortisone (Sigma, St Louis, MO, USA), 20 U/ml interleukin 2 (Boehringer Mannheim, Germany) and 120 nU/ml anti-interferon (ICN

Biochemicals, Costa Mesa, CA, USA). Cells were maintained by half medium changes every 3 to 4 days after PHA stimulation, with the addition of fresh stimulated donor PBMC on days 7, 14 and 21. Virus production was assayed for by cell-free reverse transcriptase activity (Neate *et al*, 1987) or p24 activity (Abbott Diagnostics assay).

5

EXAMPLE 2

DNA Preparation and PCR Amplification

- Non-pathogenic HIV-1 (e.g. strain C18) infected peripheral blood mononuclear cells (PBMC) were harvested 4 days after infection of phytohaemagglutinin (PHA) stimulated
- 10 HIV-1 negative donor PBMC cultured by the method of Neate *et al* (1987) and washed in phosphate buffered saline (PBS). PBMC from Donor D36 and Recipients C18, C54 and C98 were prepared by Ficoll isopaque centrifugation of buffy coat cells and washed with PBS.
 - 15 Approximately 10^7 cells were lysed in 1ml lysis solution (0.45% v/v NP40, 0.45% v/v Tween 20, 10mM Tris-HCl pH 8.3, 40mM KCl 2.5 mM $MgCl_2$) and digested with 60µg/ml proteinase K (Boehringer Mannheim) at 55°C for 1 hour followed by 100°C for 10 minutes. Lysates were stored at -20°C.
 - 20 All polymerase chain reaction (PCR) primers (Table 1) and sequencing primers (Table 2) were synthesized using an Applied Biosystems model 391 DNA synthesizer using phosphoramidite chemistry.
- Strict physical separation was maintained for sample, PCR reagent mix and PCR reaction
- 25 preparations as well as amplification and analysis. Final reaction mixes (50µl) contained 2 µl neat or diluted cell lysate, 0.2µM each primer, 200mM dNTPs and 1.25 units Taq polymerase (Boehringer Mannheim) in PCR buffer, (10mM Tris-HCl pH8.3, 50mM KCl, 100µg/ml gelatine) adjusted to the optimum $MgCl_2$ concentration for the primer pair (1.5-3.0mM). Aliquoted reagent mix was overlaid with 50µl mineral oil prior to
 - 30 addition of DNA template lysate. After template denaturation at 94°C for 3 min amplification was achieved with 30 cycles of 94°C, 1 min; 55°C, 1 min; 72°C, 2 mins. A final elongation reaction was conducted at 72°C for 7 minutes. For double PCR

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- 61 -

amplification 2 µl of first round product was added to the second reagent mix and amplified as before.

- 5 PCR amplified DNA was checked for quality, quantity and fragment size by agarose gel electrophoresis in Tris-Acetate-EDTA buffer (Sambrook et al, 1989) stained in ethidium bromide and viewed by UV transillumination.

EXAMPLE 3

DNA Sequence Analysis

- 10 The DNA sequence of PCR amplified HIV-1 regions was determined by the dideoxynucleotide method (Sanger et al, 1997) using Sequenase T7 polymerase (United States Biochemicals).

- PCR amplified DNA was purified by PCR Magic prep resin chromatography (Promega).
- 15 Approximately 2 to 7 µg purified DNA plus 10ng specific primer (Table 2) were denatured by boiling for 3 mins and snap frozen to -20°C. The initial labelling reaction was for 3 minutes at 22°C (room temperature) with ³⁵SdNTP (500Ci/mmol; Dupont) followed by dideoxynucleotide termination reactions at 37°C for 5 minutes. NP40, to 0.45% v/v, was included in denaturation and reaction mixes (Bachman et al, 1990).
- 20 Sequencing reaction products were denatured in formamide and resolved on a 6% w/v polyacrylamide gel containing 8M urea, fixed in 10% v/v acetic acid, 10% v/v methanol and dried. Following autoradiography on XK1 film (Kodak) the gel sequences were read assembled, translated to protein and aligned using the PC/GENE suite of programs (IntelliGenetics, USA).

TABLE 1
PCR PRIMERS

PRIMER	SEQUENCE ^{1, 3}	POSITION ²
CI-1	TGGAAGGGCTAATTTGGT(616)	1-18
CI-2	ATCTTCCCTAAAAAATTAGCCTGTC(617)	2099-2075
LTR-3'	AGGCTCAGATCTGGTCTAAC(618)	9559-9540
SK68	AGCAGCAGGAAGCACTATGG(619)	7786-7805
CI-6	TGCTAGAGATTTTCCACAC(620)	9709-9691
KS-2	AGTGAATAGAGTTAGGCAGG(621)	8326-8345
RT5'-v3	GTAAGACAGTATGATCAGATA(622)	2418-2438
RT3'-v2	TTGTAGGGAATTCCAAATTCC(623)	4660-4640
RT5'-v2	CAGGATCCTACACCTGTCAACATAAT(624)	2487-2506
RT3'-v1	GGGAATTCCTTATTCCTGCTTG(625)	4655-4634

1. Sequence is presented from 5' to 3' of the primer.
2. Position is according to the numbering of HIV-1 in Myers *et al* (1992).
3. SEQ ID NOs are given in parentheses.

TABLE 2
SEQUENCING PRIMERS

PRIMER	SEQUENCE ^{1, 3}	POSITION ²
KS3	CCAGAAGTTCACAATCC(626)	8570-8553
KS4	TTCTTCTAGGTATGTGGAG(627)	8753-8735
KS5	AGTGAATTAGCCCTTCCAG(628)	9093-9075
KS6	TGCTAGAGATTTTCCACAC(629)	9709-9691
SP2	TGCTCTGGAAAACATCAT(630)	8006-8022
SP3	CTTTCTATAGTGAATAGAG(631)	8318-8336
SP4	TATTGGAGTCAGGAACT(632)	8618-8634
SPR	GGTCTAACCAGAGAGAC(633)	9547-9531

1. Sequence is presented from 5' to 3' of the primer.
2. Position is according to the numbering of HIV-1 in Myers *et al* (1992).
3. SEQ ID NOs are given in parentheses.

EXAMPLE 4

Cells and Cell Culture

Peripheral blood was obtained from HIV-1 sero-negative volunteers and mononuclear cells prepared by centrifugation on a Ficoll/Hypaque density gradient (Peper *et al*, 1968). PBMC were activated with phytohemagglutinin (PHA; 10 μ g/10⁶ cells) for 48 h at 37°C washed and then cultured in RPMI 1640 medium containing 10% v/v heat inactivated foetal calf serum, 15mM HEPES, 0.1% v/v sodium bicarbonate, 25 μ g/ml polybrene (Sigma), 10% v/v interleukin 2 (Boehringer Mannheim) and 1:1000 anti-interferon (Miles) (IL-2 medium). Non-PHA stimulated cells were prepared in a similar manner except they were cultured in medium lacking PHA and IL-2.

EXAMPLE 5*Antipeptide-antisera*

Antibodies specific for HIV-1 Nef were raised against a peptide corresponding to the predicted amino acid residues 15-27 (AVRERMRRRAEPAA SEQ ID NO: 634) of Nef encoded by the HIV-1 clone pNL4.3 (Kemp et al, 1988). The peptide was conjugated to keyhole limpet hemocyanin (KLH; Calbiochem, Behring Diagnostics, CA) via glutaraldehyde and this complex used to immunise sheep (0.5mg peptide conjugate/sheep). Antibodies to the peptide were purified by affinity chromatography. Reactivity of the antibodies with recombinant HIV-1 Nef 25 and 27 was demonstrated by immunoblotting.

EXAMPLE 6*Reactivity of anti-Nef₍₁₅₋₂₇₎ with HIV C18-infected Cells in Immunoblotting*

Seven days post-infection HIV-1 C18-infected PBMCs and mock - infected cells were washed in PBS then lysed (0.5% w/v NP-40, 0.5% w/v sodium deoxycholate, 50mM NaCl, 25mM Tris-HCl, 10mM EDTA, 0.01% w/v sodium azide and 10mM phenylmethylsulphonylfluoride). After nuclei were spun out lysates were electrophoresed in a 13% w/v SDS-polyacrylamide gel (SDS-PAGE) and subsequently transferred to Hybond-C nitrocellulose (Amersham, Buckinghamshire, England) for 1 h at 100 V using a Bio-Rad protein transfer cell (Bio-Rad, Richmond, Ca). Membranes were pre-incubated with 1% w/v BSA/PBS for 2 h at room temperature and then reacted with affinity purified sheep anti-Nef₍₁₅₋₂₇₎ diluted 1:100, overnight at room temperature. After three washes in 1% w/v BSA/PBS, the blots were incubated with donkey anti-sheep Ig conjugated to biotin (Amersham, diluted 1:500) for 1 h at room temperature. After extensive washing as described above the membranes were incubated with streptavidin-conjugated horse radish peroxidase (Amersham; diluted 1:500 for 1 h at room temperature. All dilutions were made with 1% w/v BSA in PBS. After further washing the membrane was developed with phenylenediamine substrate (Dako, Dapopatts, Denmark). The antibody preparation used in the immunoblotting experiments was free of detectable antibodies to the immunogenic carrier protein and coupling reagent.

EXAMPLE 7

Analysis by Polymerase Chain Reaction Amplification

A 5' fragment defined by primers Cl-1 and Cl-2 containing the 5' LTR and part of the *gag* gene was amplified. DNA from HIV-1 C18 infected PBMC gave an amplified fragment (amplimer) of about 1.9 kb compared with 2.1kb for pHXB2 control template, implying a deletion of about 200bp from HIV C18. Further amplification of this fragment with primers defining the U3 region of the LTR (Cl-1 and LTR-3') gave amplimers of about 300 bp for HIV-1 C18 infected PBMC DNA compared with 340bp for C18 and D36 PBMC DNA and 484 bp for pHXB2 control. This implies the loss of approximately 140 to 180bp from the U3 region of these proviral DNAs.

To analyse the *nef*-gene-3' LTR region, the nested primer pairs SK68-CI-6 and KS-2-LTR-3' were used in a double PCR. Amplimers of approximately 830bp were obtained for HIV-1 C18 infected PBMC DNA as well as for PBMC DNA from Donor D36 and Recipients C18, C54 and C98 compared with approximately 1230bp for pHXB2 DNA. These results suggest that about 400bp of DNA have been deleted from the Donor and Recipient proviral DNAs.

In comparison, amplification of the polymerase gene region by double PCR with the nested primer pairs RT5'-v3-RT3'-v2 and RT5'-v2-RT3'-v1 gave a fragment (approximately 2.1 kb) the same size as the molecular clone pHXB2 fragment for HIV-1 C18 infected PBMC DNA, suggesting that deletions from this region were unlikely.

EXAMPLE 8

25 Nucleotide Sequence of the nef-3' LTR Region

PCR amplification experiments indicated an approximately 200bp nucleotide deletion from both the *nef* gene and LTR regions of Donor D36 PBMC and Recipient C18 HIV-1 proviral DNA. To further analyse these regions, the DNA sequence was determined for the PCR amplified *nef*-3' LTR region of D36 PBMC, C18 isolates HIV_{D36} and HIV_{gav} as well as isolate C98 HIV infected PBMC proviral DNA. The 3' region was amplified with outer primers (SK68-C16) and inner primers (SK68-LTR 3' or KS2-C16) and sequenced directly using a number of internal sequencing primers based on the HIV-

1_{NL43} nucleotide sequence (Table 2).

Alignment of the nucleotide sequences of the amplified 3' region of donor D36 PBMC and recipient C18 isolates HIV_{MBC} and HIV_{SV} and C98 HIV (Fig 1) showed a number
 5 of nucleotide sequences changes, including deletions, relative to the nucleotide sequence of wild-type infectious HIV-1 (HIV-1_{NL43}). In the region of alignment, D36 PBMC lacked 291 nucleotides, C18 HIV_{SV} differed in size by 388 nucleotides (comprising deletions of 397 nucleotides and an insertion of 9 nucleotides), C18 HIV_{MBC} differed by 456 nucleotides and C98 HIV lacked 158 nucleotides compared with HIV-1_{NL43}.
 10 The overall identity with HIV-1_{NL43} nucleotide sequence of D36 PBMC, C18 HIV_{SV}, HIV_{MBC} and C98 HIV nucleotide sequences, including deletions, was 73% (1157/1596), 67% (1459/1592), 62% (982/1592) and 79% (1105/1399), respectively.

The D36 PBMC sequence differed from HIV-1_{NL43} in a number of features. A change
 15 in the wild type *tar* termination codon from TAG to TCG (Ser) extended the third *tar* exon (which starts at splice acceptor 10) by a further 15 amino acids to terminate at a conserved TAG (Fig 1). The resulting C-terminal peptide is rich in charged amino acids (8/15) (Fig 2a). The wild type *rev* termination codon has also changed (TAG to GAG, Glu) and the third *rev* exon is extended for 14 codons to terminate at a conserved TAG
 20 (Fig 2b). The encoded extra amino acids are mainly polar (11/14) and charged in nature (Fig 2b). The sequence also encodes the C-terminal 237 amino acids of Env gp41 (Fig 3) terminating at the normal termination codon. The D36 PBMC Env amino acid sequence has 85% identity with the HIV-1_{NL43} sequence, increasing to 89% if similarities are included.

25

There are significant differences from HIV-1_{NL43} downstream of the *env* (gp41) gene. A change in the fifth *nef* codon, from TGG (Trp) to TGA (Fig 1), introduces an early termination in the D36 PBMC *nef* gene. The encoded Nef protein is identical to the N-terminal 4 amino acids of HIV-1_{NL43} Nef (Fig 4). Following the early termination there
 30 are deletions of 33, 47, 93 and 91 nucleotides and a region of low sequence homology, compared with HIV-1, prior to the wild type *nef* termination codon site (HIV-1 nts 9405-9407). As well as removing a significant part of the *nef* gene, these deletions also

bring into phase a further 6 termination codons. While the polypurine tract (plus strand primer binding site) and the first 38 nucleotides of the LTR U3 region are perfectly conserved, downstream U3 region sequences are disrupted by the 93 and 91 nucleotide deletions and the low homology region. The resulting U3 region lacks recognition
5 sequences for the transcription factors *c-myb*, USF and TCF1 α as well as one of the suggested NF-AT sites (Gaynor et al, 1992). Downstream from the 91 nucleotide deletion, a 59 nucleotide region of low homology contains two extra NF κ B enhancer sites 19 nucleotides upstream of the usual site of a pair of NF κ B sites, the upstream one of which is altered in its 5'-half in D36. Sequences further downstream are highly
10 conserved with respect to HIV-1_{NL43}, including the position and number of Sp1 basal promoter sites, TATA box, TAR and polyadenylation signal sequences.

Similar to D36 PBMC, the C18 HIV_{SV} and HIV_{MBC} sequences show the *tat* third exon to be extended by 15 codons. All but two codons (altered by point mutations) are
15 identical to those of D36 PBMC (Fig 2a). The *rev* third exon of both C18 isolates is also extended (Fig 2b) but by only three codons, identical to the first three codons of the D36 PBMC *rev* extension. The same 237 amino acid coding region of Env gp41 is found in both the C18 HIV DNA sequences (Fig 3) and shows 85% identity, increasing to 88% if similarities are included, with the same region of the HIV-1_{NL43} Env gp41.

20 It is in the *nef* gene and LTR regions that the major differences from wild-type HIV-1 arise, just as in D36 PBMC. The *nef* gene of C18 HIV_{SV} encodes 24 amino acids with 9 of the 10 N-terminal being identical to the HIV-1_{NL43} Nef protein (Fig 4). Thereafter, deletions of 177 and 11 nucleotides cause a frameshift and termination at the 25th codon
25 (Fig 1). Downstream deletions of 120, 82 and 7 nucleotides cause further loss of wild type *nef* gene sequence and bring into phase a further three termination codons.

The *nef* gene of C18 HIV_{MBC} encodes only 7 amino acids with only the initiator methionine identical to the HIV-1_{NL43} Nef protein. This loss of identity and early
30 termination is brought about by a 250 nucleotide deletion after the fifth nucleotide of the *nef* gene. Downstream deletions of 120 and 86 nucleotides cause further loss of wild-type *nef* gene sequences. In both C18 isolates there is perfect conservation of the

- 68 -

polypurine tract and 29/31 nucleotides at the 5' end of the U3 region immediately before the 120 nucleotide deletion (Fig 1). This deletion together with the downstream 82 and 7 nucleotide deletions in HIV_{SV} and 86 nucleotide deletion in HIV_{MBC} and the low homology region cause the loss of the 5' half of the NRT-1 site (Yamamoto et al 1992) and the downstream NFAT site. A third NFkB site is present 31 (HIV_{SV}) and 33 (HIV_{MBC}) nucleotides upstream of the expected pair of NFkB sites which are themselves separated by 13 nucleotides instead of the 4 nucleotides in HIV-1_{NL43}. The 5'-most Sp1 site sequence is slightly altered but sequences downstream including the other 2 Sp1 sites, the TATA box, TAR and polyadenylation signal sequences are identical to HIV-1_{NL43} sequence.

The three sequences, D36 PBMC, C18 HIV_{SV} and C18 HIV_{MBC} show a number of similarities consistent with the transmission of virus from person D36 to person C18 as well as a number of differences indicating post-transmission divergence of sequence. All three have *tat* open reading frames (ORFs) extended by 15 codons. All three have extended *rev* ORFs. The new *rev* termination codon in both C18 HIV-1 isolates, three codons downstream of the HIV-1_{NL43} *rev* termination codon, has a point mutation in D36 PBMC to make a Glu codon so that it continues for a further 11 codons (Fig 2b) to terminate at a conserved TGA. The partial Env gp41 amino acid sequences are more closely related to each other (86% identity or 90% including similarities) than to HIV-1 (85% and 89%, respectively).

The nucleotide sequence of the *nef* and LTR region of the HIV-1 isolate from recipient C98 (C98 HIV) is 90.3% identical (1264/1399) to the HIV-1 sequence, ignoring deletions. Similar to the D36 PBMC and C18 HIV_{SV} and HIV_{MBC} isolates the C98 HIV sequence shows the third exon of *tat* to be extended by 15 codons with all but one being identical to the D36 PBMC *tat* extension. Also, the *rev* gene is extended by 3 codons, 2 of which are identical to the first 2 codons of the D36 PBMC *rev* extension. The sequence also encodes the C-terminal 223 amino acids of Env gp41 terminating at the normal termination codon. The C98 HIV Env amino acid sequence has 89% identity with HIV-1 Env sequence, increasing to 92% of similarities are included.

- As with the D36 PBMC and the C98 HIV isolate sequences it is the *nef* gene and LTR regions that major differences from the HIV-1 sequence arise. The *nef* gene open reading frame of C98 HIV is much longer than in D36 PBMC, C18 HIV_{SV} and HIV_{MBC}, encoding 85 amino acids compared with 206 amino acids for HIV-1_{NL43}.
- 5 Sixty eight of those 85 amino acids are identical to the N-terminal sequence of HIV-1_{NL43} Nef. The single, small deletion (16 nucleotides) in the C98 HIV *nef*-alone regions (Table 3) occurs after *nef* codon 82, causing a frameshift and termination after a further 3 codons at the start of the highly conserved polypurine tract sequence immediately before the 3'-LTR. The *nef*/LTR region has two deletions totalling 142 nucleotides.
- 10 The 5'-most deletion of 42 nucleotides includes the splice acceptor 12 sequence. The NRT-1, dyad symmetry and *myb* response element sequences are all intact. However, the downstream 100 nucleotide deletion includes sequences from the 3' end of the 5'-NF-AT and all of the 3' NF-AT sequences as well as the USF transcription factor recognition sequence. The downstream low homology region of 77 nucleotides lacks
- 15 the TCF-1 α sequence but has two additional NF κ B sites 13 nucleotides apart and 26 nucleotides upstream of the 3'-half-remnant of the normal 5'-NF κ B site. Sequence downstream, including the 3'-NF κ B site, the 3 S ϕ I sites, TATA box TAR and polyadenylation signal sequences are all highly conserved.
- 20 The main feature of the sequences is the series of deletions, with respect to HIV-1, in the *nef* gene-3'-LTR region. These can be grouped into two regions namely the *nef*-alone region, that part of the *nef* gene upstream of the LTR, and the *nef*/LTR region, where the *nef* gene and LTR U3 regions overlap. The deletions in these regions of each of the sequences start and end at the same or similar positions (Table 3). The deletions
- 25 are larger in C18 HIV_{SV} and C18 HIV_{MBC} sequences where totals of 397 and 456 nucleotides have been deleted (relative to HIV-1_{NL43}) compared to 291 nucleotides, from D36 and 158 nucleotides from C98 HIV. In the *nef*-alone region the two deletions in C18 HIV_{SV} and the single deletion in C18 HIV_{MBC} occupy the same region as the three deletions in D36 PBMC. Similarly, the *nef*/LTR region in the three deletions in the C18
- 30 HIV_{SV}, the two deletions in the C18 HIV_{MBC} and the D36 PBMC sequences occupy the same region. These findings indicate that mutant virus was transmitted from D36 to C18 after which further deletions and rearrangements occurred. Similarly, the

sequence of C98 HIV in the *nef*/LTR region indicates two deletions occupying the same region as the *nef*/LTR deletions in D36 and the C18 sequences. However, the size (only 16 nucleotides) and the position of the deletion in the *nef*-alone region of C98 HIV are distinct from those of the D36 PBMC and C18 sequences.

5

The timing of transmission of virus by transfusion was that recipient C18 was transfused approximately 19 months after C98. Consistent with the relative timing of transmission and the sequence similarities and differences is the suggestion that at the time of transmission to C98, the D36 sequence had deletions in the *nef*/LTR region but not in
10 *nef*-alone region. After transmission to C98, the C98 virus developed further deletions and rearrangements, including the deletion in the *nef*-alone region. The D36 virus evolved so that at the time of transmission to C18, further deletions and rearrangements had occurred including deletion of sequence from the *nef*-alone region distinct from the C98 HIV *nef*-alone region deletion. After transmission to C18, further deletions and
15 rearrangements occurred in the C18 virus giving rise to at least two sequences (HIV_{SV} and HIV_{MBC}).

The *nef*-alone deletion region may be a mutation or recombination "hotspot" as it includes sequences that were found to be variably duplicated in 28 out of 54 Nef protein
20 sequences derived from 8 of 12 patients analysed in a study (Shugars *et al* 1993). The sequence between the *nef*-alone and the *nef*/LTR region deletions is highly conserved and is important in provirus integration into the infected cell genome and interacts with a number of cellular proteins. It is interesting that the sequence equivalent to HIV-
1_{NL43} nucleotides 9209 to 9225 is retained in D36 and C98 HIV but lost in the C18
25 HIV sequences. This includes part of a sequence of dyad symmetry (9210 to 9231) and is a significant part of the binding site for NRT-1 (Yamamoto *et al* 1991) which has been shown to have a negative regulatory effect on HIV-1 expression. The presence of this sequence in D36 and C98 HIV and its absence from the C18 isolates may correlate with the inability to isolate virus from D36 PBMC and the poor replication of C98 HIV
30 but the ability to isolate HIV-1 from C18 PBMC. The deletion of sequence equivalent to nucleotides 9281 to 9395 of HIV-1_{NL43} causes the loss of some transcription factor binding sites including NFAT and USF from the D36, C18 HIV and C98 HIV sequences.

A further similarity between the D36, C18 HIV_{SV}, C18 HIV_{MBC} and C98 HIV sequences is a region of low homology to HIV-1_{NLA3} extending downstream of the *neff*LTR deleted region to the NFkB enhancer/Sp1 promoter site region. This low homology region in fact consists of incomplete duplications of part of the NFkB/Sp1
 5 region (Fig 5) resulting in D36 and C98 HIV having 2 extra NFkB sites upstream of an altered 5' NFkB site while the C18 sequences have one extra NFkB site and altered spacing between the 5' and 3' wild type NFkB sites due to an insertion of 9 nucleotides.

For the C18 and C98 HIV-1 isolates virus replication was assessed in PHA-stimulated
 10 and non-stimulated PBMCs (Figs 6 and 7). In PHA-stimulated PBMCs we also studied cell surface CD4 and IL-2R expression (Fig 8). In comparison with HIV-1 wild-type SI and NSI isolates clearly both C18 HIV_{MBC} and C98 viruses are replication competent, though C98 HIV replicates more poorly than C18 HIV_{MBC} and are of the NSI phenotype when syncytium formation and CD4 and IL-2R surface expression are
 15 taken into account. Additionally, and more surprisingly, these two viruses replicated almost as efficiently in non-PHA stimulated PBMCs when compared to a typical local wild type SI isolate (HIV-1 228200, Fig 7).

When protein expression was assessed for C18 HIV_{MBC} and C98 HIV_{MBC} although
 20 structural proteins were identified, no typical Nef protein was seen in infected cells. However, analysis of cell lysates prepared from PBMC infected with C18 HIV_{MBC} or PBMC infected with C98 HIV_{MBC} (which were subsequently stimulated by UV irradiation, see Valerie *et al*, 1988) by Western immunoblotting using two antibodies specific for the N-terminal region of Nef showed the presence of smaller proteins of 19
 25 kDa and 21 kDa, respectively. These proteins were not observed in mock-injected control PBMC lysates and were not observed when the infected-cell lysates were probed were probed with antibodies reactive with the C-terminus of Nef.

Thus, although the C18 and C98 HIV isolates are replication competent *in vitro* they
 30 clearly replicate differently using different conditions for cell activation and from the known functions of HIV-1 Nef protein and the LTR show that the major deletion in the *nef* gene and/or the LTR is at least in part responsible for the outcome of infection,

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- 72 -

implicating the importance of Nef and/or the LTR in the clinical outcome of infection *in vivo*.

EXAMPLE 9

5 *Determination of Degree of Relatedness Between Viruses*

To determine the degree of relatedness between viruses such as between mutants or between mutants and a wild-type virus and to ascertain putative infected patients, the method of Delwart *et al* was employed.

10 EXAMPLE 10

Immune responsiveness of subjects infected by non-pathogenic HIV-1 isolate

In this example, the donor and recipients of the cohort were tissue typed and assessed for basic cellular immune responses. Proliferative responses and IL-2 production to the mitogens ConA and PHA, to allogeneic mononuclear cells (irradiated pooled
15 mononuclear cells from 20 random donors) and to recall antigens (e.g. influenza and tetanus toxoid) were within normal ranges. While at the immunogenetic level, HLA typing failed to identify a consistently common allele or haplotype within the group.

The conservation of CD4+ counts observed in the cohort, the relative integrity of their
20 immune system and the varied HLA types of the donor and recipients further supports the fact that the symptomless condition of the cohort members is due to a non-pathogenic strain of HIV-1 or a strain of low virulence.

Accordingly, this provides a screening procedure for subjects putatively infected by a
25 non-pathogenic HIV-1 isolate where such subjects are seropositive for HIV-1 (e.g. have antibodies to an HIV-1 glycoprotein) yet have normal proliferative responses and cytokine production to mitogens, allogeneic mononuclear cells and to recall antigens.

EXAMPLE 11*Clinical Immunology of Cohort*

To establish that the donor and the recipients belonging to the cohort exhibit normal immunological profiles, members of the cohort were assayed for CD3, CD4, CD8, lymphocyte count, CD4/CD8 ratio and β -2-microglobulin over time since seroconversion.

Parameters considered normal in non-infected individuals range as follows:

<u>Parameter</u>		
CD3	55-82%	620-2200 ($\times 10^6/L$)
CD4	29-58%	420-1410 ($\times 10^6/L$)
CD8	12-43%	200-980 ($\times 10^6/L$)
Lymphocyte count	1000-3500 ($\times 10^6/L$)	
CD4/CD8	0.7-3.7	
β -2-microglobulin	0.00-2.20 mg/L	

The results are shown in Figures 10(a)-(g) and clearly show that the immunological profiles of cohort members are substantially normal further highlighting the non-pathogenicity of the HIV-1 isolates of the present invention. Figure 10(g) shows a graph of the Kaplan-Meier (Ox and Oates, 1989) estimates of time to disease progression (AIDS or $CD4 > 250$). The results demonstrate that the difference is large in spite of the conservative bias, with a median time to progression of 6.2 years in the main database. An exact logrank test (Cytel Software Corporation, 1989, StatXact: Statistical Software for Exact Nonparametric Inference. Cambridge, Massachusetts.) was performed, demonstrating that the difference between the groups was highly statistically significant (logrank statistic 11.8, $p < 0.0001$).

Table 3
Deletions and their sizes in the *nef*-alone and the *nef*/LTR regions of the Long-Term Asymptomatic HIV-1 Sequences

Sequence	<i>nef</i> -alone Region	Region Deletion (nt)	<i>nef</i> /LTR Region	Region Deletion (nt)	Total Deletion (nt)
D36 PBMC	8830-8862 (33)		9112-9204 (93)		
	8882-8928 (47)		9281-9371 (91)	184	291
	9009-9035 (27)	107			
C18 HIV _{SiV}	8830-9006 (177)		9105-9224 (120)		
	9019-9029 (11)	188	9281-9362 (82)	202	390
C18 HIV _{MBC}	8792-9041 (250)	250	9105-9224 (120)		
			9281-9366 (86)	206	456
C98 HIV	9033-9048 (16)	16	9148-9189 (42)		
			9271-9370 (100)	142	158
C54 PBMC	incomplete	?	9281-9375 (95)	95	95 +

Sequence numbering relates to the equivalent position in HIV-1 NL4-3. Numbers in brackets are the deletion sizes in nucleotides (nt).
 The *nef* ORF starts at nt 8787 and the 3'-LTR starts at nt 9074 in HIV-1 NL4-3.

EXAMPLE 12

Sequencing of isolate HIV-1 C18_{MBC}

The genome of variant HIV-1 designated C18 HIV-1_{MBC} was amplified by the
 5 polymerase chain reaction (PCR) as 7 overlapping fragments using the sets of inner and
 outer oligonucleotide primers, designed using the programme PCRPLAN
 (IntelliGenetics), listed in Table 5 and either UITma (Applied Biosystems) or a mixture
 of KlenTaq and Pfu (KlenTaq LA, Ab Peptides Inc) polymerases (for faithful
 amplification of long fragments). The resulting fragments were cloned into the SmaI
 10 site of the plasmid vector pGEM7Zf+. Insert-containing clones representing each region
 of the full length variant HIV-1 were sequenced by a nested deletion strategy (Gou &
 Wu, 1982) and cycle sequencing with Taq polymerase and dye labelled primers
 complimentary to the T7 or SP6 sites within the cloning vector. Nucleotide sequences
 were entered and collated by ASSEMBL and SEQIN (IntelliGenetics) and SEQED
 15 (Applied Biosystems) and translated to the encoded amino acid sequences using
 TRANSL (IntelliGenetics) programmes. Sequence alignments used NALIGN,
 CLUSTAL (IntelliGenetics) and SEQED programmes.

The full length sequence (Fig 9; SEQ ID NO:800) of isolate HIV-1 C18_{MBC} is 9207
 20 nucleotides long which is 506 nucleotides shorter than the HIV-1 sequence. This size
 difference is comprised of 126 nucleotides of insertions and 632 nucleotides of deletions,
 see Table 6. The most extensive differences between the HIV-1 C18_{MBC} sequence and
 HIV-1_{NL43} are in the U3 region of the LTR and in the *nef* gene, as hereinafter
 described.

25 The 5' LTR has deletions of 120 and 87 nucleotides and a region of low sequence
 homology, which is the result of an imperfect duplication of the downstream NFκB and
 Sp1 response sequences. These result in the loss of sequence from a number sites
 important in the regulation of transcription of HIV-1 genes, including the negative
 30 response element (NRE) and the response elements for a number of transcription factors
 including NF-AT, NRT-1, USF and TCF-1α. Furthermore, the low homology region
 contains an extra NFκB and Sp1 sites as well as an insertion of 9 nucleotides between

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the usual NF κ B sites. Downstream of the NF κ B sites the sequence of the LTR has a high level of homology (96.2%) with the same region of HIV-1.

The *gag* gene contains 3 insertions, which represent direct repetitions of adjacent sequences. The first is a perfect repeat of 15 nucleotides after the equivalent of nucleotide 1134 of HIV-1_{NL43} and adds 5 amino acids to the C-terminus region of p17²⁴⁶. The remaining 2 insertions are imperfect and perfect repeats of 30 and 6 nucleotides, respectively, after the equivalent of HIV-1 nucleotides 2163 and 2232, respectively. These encode an extra 12 amino acids in the C-terminus region of p15²⁴⁶ just downstream of the *gag* to *pol* frameshift sequences. The variation in sequence length of the *gag* gene at these two positions is unusual. The homology of the encoded amino acid sequence of HIV-1 C18_{MBC} and HIV-1 for the *gag* p17, p24, and p15 proteins is 87.1%, 93.5% and 94.3%, respectively.

In the *pol* ORF, the encoded proteins have high homology with the HIV-1_{NL43} sequences being 95.5% overall comprising p10 protease 92.9%, p66 reverse transcriptase 95.4% and p34 integrase 95.8%. The amino acid sequence of the p61 RT lacks the mutations associated with resistance to the nucleoside (AZT, ddI, ddC) and non-nucleoside (Nevirapine) analogue drugs used in the treatment of HIV-1-infected persons.

The *vif* gene encodes a 192 amino acid protein with 88.0% homology with that of HIV-1. The *vpr* gene encodes a 96 amino acid protein with 89.6% homology with that of HIV-1_{NL43}.

There are 2 insertions and 1 deletion of sequences in the *vpu* gene. The insertions of 3 and 9 nucleotides are after the equivalent of nucleotide 6071 and 6234, respectively, of HIV-1_{NL43}. These add 1 amino acid after amino acid 3, and 3 amino acids after amino acid 59 of the encoded *Vpu* protein. The deletion of 12 nucleotides after the equivalent of HIV-1_{NL43} nucleotide 6261 deletes 4 amino acids from the C-terminal region of *Vpu* as well as from the signal peptide of the *env* polyprotein, which is encoded by an overlapping reading frame. Amino acid sequence homology of HIV-1 C18_{MBC} *Vpu* with HIV-1_{NL43} is 85.2%.

- 77 -

The sequence encoding the *env* gp120 has 9 insertions totalling 45 nucleotides (encoding 15 amino acids) and the deletion of a total of 18 nucleotides (encoding 6 amino acids). These are listed in Table 6. All of these events (insertions and deletions) are at positions in the *env* gene. This is within the *env* V3 coding region, immediately upstream of the sequence encoding the so called V3 tip (or loop) amino acid sequence, Gly Pro Gly Arg. The V3 region sequence is that of a typical clade B subtype (North America, Europe and Australia) being identical to the clade B consensus sequence (based on 186 *env* sequences) at 29/35 positions. The type of amino acid at positions 11 and 28 of the V3 loop region (where position 1 is the Cys at amino acid 266 of the *env* gp120) is predictive of the viral non-syncytium / syncytium forming phenotype (Fouchier et al, 1992). The HIV-1 C18_{MBC} *env* gene encoded amino acid sequence has Ser at position 11 and Ile at position 28 of the V3 loop region. The lack of a positively charged amino acid at both positions is strongly indicative of a non-syncytium viral phenotype. The overall amino acid sequence homology with HIV-1_{NL43} (ignoring deletions and insertions) is 86.1%, comprising 85.5% for the gp120 region and 87.6% for the gp41 region.

Both the *tat* and *rev* second exon open reading frames (ORF) are longer than in HIV-1_{NL43}. A change of the *tat* termination codon from TAG to TCG extends the *tat* ORF to a downstream in phase termination codon extending the encoded *tat* amino acid sequence by 15 residues, compared with the 86 amino acid long HIV-1_{NL43} *tat* protein, to a total length of 101 amino acids. However, this is the usual length of the HIV-1 *tat* protein.

Similarly, the normal *rev* termination codon is changed from TAG to GAG. This extends the *rev* ORF to an in-phase termination codon 3 codons downstream so that the encoded Rev protein is 119 amino acids long instead of the usual 116.

As mentioned above the most extensive differences between the sequences of the isolate HIV-1 C18_{MBC} and HIV-1_{NL43} are in the *nef* gene and the LTR region. While the *nef* gene overlaps the 3' LTR, these differences are found in both the *nef* alone and the *nef* / LTR overlap regions. The HIV C18_{MBC}-encoded *nef* protein is only 24 amino acids

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long compared with the normal length of 206 amino acids. This severe shortening of the *nef* protein is due to the deletion of 188 nucleotides (the 177 and 11 nucleotide deletions) from the *nef*-alone region which also brings into phase a termination codon, TAG, at the resulting 25th codon. Downstream there is further loss of potential *nef* gene sequences by the 120 and 87 nucleotide deletions situated in the *nef* / LTR overlap region. The resulting 24 amino acid *nef* protein is identical to the N-terminus of the HIV-1_{NL43} *nef* at 9 of the first 10 positions. Thereafter, homology is lost completely.

Some sequences used in the generation of mature mRNAs are altered or lost in C18_{MBC}.
 10 The dinucleotide immediately after the splice donor site 2 (SD2) at nts 4818-4819 (HIV-1_{NL43} equivalent nts 4963-4964) is changed from the conserved GT to GC. It is expected that this change would lead to loss of function of this site as a splice donor. Splice donor 2 is used in the processing of HIV-1 transcripts to some of the mRNAs that encode Tat, Rev and *nef* proteins. Similarly the splice acceptor site 7 (SA7) sequence
 15 at nts 6477-6478 (HIV-1_{NL43} equivalent nts 6602-6603) is changed from the conserved AG dinucleotide to TC. This change is expected to lead to loss of function of this site as a splice acceptor. While this SA site is used in HIV-1 mRNA processing it is not a major site and is not used in the production of the regulatory proteins (Tat, Rev or *nef*) mRNAs. The splice donor 12 site is absent from the C18_{MBC} sequence (NL43
 20 equivalent nts 9161-9162) as it is within the first deletion region in the *nef* / LTR overlap region which occurs at nt 8797 and results in the loss of NL43 nucleotides 9105 to 9224. It is significant that the SA12 site is absent from the sequence of all of the cohort virus isolates so far obtained as well as from the sequence of D36 PBMC, however, the C54 PBMC sequence does contain the SA12 site. SA12 is not used in the
 25 processing of mRNAs that encode the viral regulatory proteins. Normally SA12 is used in splicing in conjunction with SD1, 2, 3 and 4 and the resulting spliced RNA is probably not a mRNA but may have a regulatory role involving binding to cellular proteins (Smith et al, 1992).

30 An interesting feature of the sequence of the HIV-1 C18_{MBC} isolate is the deletion and rearrangement of sequence from the 5'-LTR U3 region and the deletion of sequence from the *nef* gene (both *nef* alone and *nef* / 3' LTR regions). These being the only

- 79 -

features of the sequence distinct from disease-causing HIV-1. The lack of AIDS or AIDS-like symptoms in the patient C18 is attributed to the effects of the loss of LTR sequence and / or the loss of *nef* coding sequences and their role in the pathogenesis of AIDS.

5

TABLE 4
Primers used to Amplify Overlapping regions of HIV-1 C18_{MBC}

10	Primer	5' - Coordinate	Direction (+/-)	Primer Length	(nt)	Sequence
15	CL 1A	1	+	30		TGAAAGGCGTAAATTTACTGCCAAAAAGAC
	CL 14	896	-	25		AATCGTTCTAGCTCCCTGCTTGGCC
	CL 1B	1	+	30		<u>AATCGCGGTTCGAAAGGCGTAAATTTACTGCC</u>
	CL 13	796	-	31		<u>CCACTAGCCGCTTAATACTGAGCGCTCTGCC</u>
20	CL 11	682	+	23		TCTCTGAGCGCAGGACTGGCTT
	CL 16	3440	-	20		CTGTTTCTGCGGTTCCTAGCTCTGCTTCT
	CL 12A	732	+	26		<u>TTTCCGCGCGCGGACTGGTGGATAC</u>
25	CL 17	3330	-	32		<u>CCCTCTAGACTTGGCCAAATTCATTTTCCAC</u>
	CL 26	3193	+	39		GCACACCGGCGAAAGCGTGGGAGGAGAGCGGCGATTC
	CL 6B	9671	-	39		TGCTAGAGATTTTCCGCGCGGCTTAATGGTCTGAGGG
30	CL 27	3251	+	39		CGATCTGATTAATGGAGGCTGCGAGCGGCTGACTGCC
	CL 28	639	-	27		TGCGCCAAACATTAATGACTCTGCATCATATGC
	CL 19	5448	+	30		AGCAGGACATACAGGTAGGATCTCTACA
	CL 24	8422	-	28		GGATCTGTCTCTGTCTCTCTCGAAGT
35						

Underlined sequences depict added restriction enzyme site

+ and - orientations refer to sense and antisense strands of the double stranded DNA sequence

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TABLE 5
Sequence Deletions and Insertions in HIV-1 C18_{MBC}
Compared with HIV-1_{NL43}

5	Gene or Region	Position (nt)		Deletions (nt)	Insertions (nt)
		C18 _{MBC}	NL43		
10	5'-LTR U3	29	29	120	-
	5'-LTR U3	85	205	87	-
	5'-LTR U3	154	360	-	9
	<i>gag</i> p17	939	1134	-	15
15	<i>gag</i> p15	1982	2163	-	30
	<i>gag</i> p15	2081	2232	-	6
	<i>vpu</i>	5927	6062	-	3
	<i>vpu/env</i>	6092	6234	-	9
	<i>vpu/env</i>	6128	6261	12	-
20	<i>env</i>	6483	6628	-	6
	<i>env</i>	6514	6653	2	-
	<i>env</i>	6524	6665	1	-
	<i>env</i>	6630	6772	-	9
	<i>env</i>	6646	6778	-	3
25	<i>env</i>	7011	7141	6	-
	<i>env</i>	7140	7276	3	-
	<i>env</i>	7195	7334	-	6
	<i>env</i>	7266	7399	3	-
	<i>env</i>	7278	7414	-	6
30	<i>env</i>	7290	7420	-	2
	<i>env</i>	7300	7429	-	1
	<i>env</i>	7314	7441	3	-
	<i>env</i>	7463	7593	-	3
	<i>env</i>	7471	7598	-	9
35	<i>nef</i>	8711	8829	177	-
	<i>nef</i>	8723	9018	11	-
	<i>nef</i> / LTR	8798	9104	120	-
	<i>nef</i> / LTR	8854	9280	87	-
	LTR U3	8923	9435	-	2
40				<u>522</u>	<u>126</u>

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EXAMPLE 13***Macrophage Isolates of HIV-1 C18 and HIV-1 C98***

- 5 HIV-1 has been isolated from the macrophages of patients C18 and C98.

Patient monocytes were prepared as follows. Whole blood was spun at 2000rpm for 10 minutes. Plasma was removed into a separate tube and the remaining cells were diluted 1:2 in PBS⁻ (magnesium and calcium free phosphate buffered saline). This was
10 underlaid with 10 ml of Ficoll Isopaque and spun at 2000rpm for 20 minutes. Cells were collected from the interphase and washed three times with PBS⁻. These cells were then seeded into a 6 well Costar tray at a concentration of 1.0×10^7 /ml and allowed to adhere for 1 hour. Any non-adherent cells were removed by aspiration.

- 15 Donor HIV-1 negative macrophages for use in co-cultivation were prepared as follows. Peripheral blood mononuclear cells were purified from whole blood using Ficoll/Isopaque density gradient. These cells were seeded at a concentration of 2.0×10^6 /ml in teflon. PBMC were cultured in the presence of $3\mu\text{g/ml}$ of PHA and 1000U/ml of M-CSF 3 days prior to co-culture.

20

- On day of co-culture, donor PBMC were CD8 depleted. Dyna beads coated with anti-CD8 were used for this purpose. Dyna beads were washed once in PBS⁻ and then applied to a magnet for 3 minutes. Supernatant was removed and the beads were then resuspended in 250 μl of RF-10. Aliquots of 2.0×10^8 patient cells were then added to
25 250 μl (3 beads : 1 CD8 T-cell) of Dyna beads and allowed to incubate for 30 minutes on ice with occasional mixing. After 30 minutes the cell suspension was placed onto a magnet for 3 minutes. The supernatant was then removed placed into a second tube containing 142 μl (1 bead : 1 CD8 T-cell) of Dyna beads. This suspension was placed on ice for an additional 30 minutes with occasional mixing. After 30 minutes cell
30 suspension was placed onto a magnet for 3 minutes. Supernatant was removed and washed once in RF-10.

For co-culture, CD8 depleted PBMC were then added to patient monocytes. Half media changes were done every 7 days for a period of 21 days. Aliquots of 2.5 ml of medium was removed from these cultures and replaced with CD8 depleted donor PBMC in Iscoves containing 10% HuS (Human serum), 5% v/v FCS and 5% w/v IL-2 and
 5 1000U/ml of M-CSF. Harvested supernatants were spun at 1400 rpm for 10 minutes and stored as 1ml aliquots. Cell pellets were lysed in 200µl of lysis buffer for PCR analysis. Infection was quantitated using a p24 EIA Kit.

Cells were harvested from the co-cultures and used to prepare DNA as described above.

10 The *nef* / 3'-LTR region of both virus isolates was amplified by PCR using the above described primer sets and conditions (Example 12). The resulting amplimers were cloned into the plasmid vector pT7T3U19 and the nucleotide sequence determined by the Taq cycle sequencing method with dye-labelled primers.

15 The C18 macrophage sequence has 3 deletions starting and finishing at positions within 3 nucleotides of the same deletions in C18_{MBC}. The encoded *nef* protein is 3 amino acids long compared with 7 amino acids for C18_{MBC}. The low homology region of the LTR U 3 region of C18 macrophage is very similar in sequence to C18_{MBC} and similarly it has one extra upstream NFκB site.

20

On the other hand, the sequence of C98 macrophage has a number of differences from the C98 isolate. While it has exactly the same first deletion of 16 nucleotides just upstream of the polypurine tract (PPT), in the *nef*-alone region, and exactly the same second deletion (position and size) it has an extra deletion of 18 nucleotides at HIV-

25 1_{NL43} equivalent nucleotides 9206 to 9223. The final deletion is in approximately the same position as in the C98 isolate but is 5 nucleotides longer. The encoded *nef* protein is 34 amino acids long compared with 86 amino acids for the C98 isolate. The low homology region is very similar to the C98 isolate, having the same 2 extra upstream NFκB sites and completely lacking the normal 5'-NFκB site.

30

EXAMPLE 14

Construction and Use of an Infectious Molecular Clone

5 Molecular biological techniques can be used to construct a molecular clone of, for example, HIV-1 C18_{MBC}. Two schemes may be used. In the first scheme genomic DNA, extracted from either the CD4 positive PBMC of the patient C18 or donor PBMC that have been infected with the isolate HIV-1 C18_{MBC}, is used as the template for polymerase chain reaction amplification, using thermostable polymerase of high
10 transcriptional fidelity (eg UITma polymerase or KlenTaq/Pfu polymerase mixture), of long (6 to 7 kb) overlapping fragments representing the 5'- and 3'-parts of the HIV-1 C18_{MBC} proviral genome of total length 9207nts. The amplified fragments may then be ligated together after digestion with a restriction enzyme that cleaves at a unique site common to the overlapping region of the amplified fragments, for example the unique
15 Bgl I or Nco I sites. Ligation of this full length proviral DNA into a plasmid vector will allow its propagation in *E coli* and the subsequent preparation of large (mg) quantities of this molecularly cloned proviral DNA.

In the second scheme donor PBMC that have been infected with the isolate HIV-1
20 C18_{MBC} are used as a source of non-integrated proviral DNA which can be extracted from the infected cells by the Hirt extraction method (Hirt, 1967). Circular proviral DNA molecules may be linearised by digestion with a restriction enzyme that cleaves at a unique position in the genome (eg the Bgl I or Nco I sites). The resulting linearised molecules can be ligated into a plasmid or, more usually, a bacteriophage lambda (λ)
25 based vector (eg Charon 4a, λ WES) after modification of the end to provide blunt or cohesive ends compatible with the vector. Transformation or transduction of *E coli* with the recombinant plasmid or bacteriophage material, respectively allows the propagation of the proviral DNA. Clones of *E coli* containing proviral DNA may be selected and DNA prepared. Molecular clones of retroviral genomes prepared in this way are often
30 permuted. Rearrangement to the functional arrangement of sequences is achieved by restriction enzyme cleavage and religation of fragments to reconstruct the correctly permuted proviral genome.

The molecularly cloned DNA products of both schemes can be used to prepare variant proviral genomes that may be used as the basis of a biologically attenuated HIV-1 vaccine strain. Similarly, they may be modified to contain extra DNA sequences in the *nef*-alone deletion region that may deliver sequences that may be of therapeutic
5 advantage (eg antisense or ribozyme sequences).

Infectious virus particles of HIV-1 C18_{MBC}, or modified virus, can be produced by transfection of human cells (eg HeLa cells) which will produce, and release to the culture medium, virus particles of HIV-1 C18_{MBC}, or modified virus. These virus
10 particles can be used to infect a variety of CD4 positive cells for further propagation or experimentation.

EXAMPLE 15

In vivo Primate Model

15 Following construction of infectious molecular clones of the mutant HIV-1 strains, studies are then undertaken in primates to establish attenuation, immunogenicity and vaccine prophylactic efficacy. All studies compare mutant clones of HIV-1 with isogenic wild-type (WT) virus. Initial studies are performed using the macaque (*M. nemistrina*) model of HIV-1 infection. Macaque-infectious WT HIV-1 and mutant
20 clones are compared with respect to duration of viremia, anatomic sites of replication, and cellular and humoral immune responses. Where the mutant HIV-1 clones induce an immune response in the macaques infected, challenge studies with WT virus are also performed. Studies are performed in a limited number of chimpanzees, generally in parallel with the macaque studies. Relevant mutations are engineered into WT HIV-1
25 clones previously shown to produce chronic infection in chimps, and the course of chimp infection with mutant clones compared with historical controls. If infection is established, WT challenge studies is also performed.

Examples 16 to 21 relate to the screening of antibodies in HIV-1 infected individuals
30 to peptides covering regions of Nef.

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EXAMPLE 16*Study Subjects*

Serum samples were obtained from seven HIV+ve individuals, D-36, C-124, C-98, C-64,
5 C-18, C-49 and C-54. Individuals C124, C-98, C-64, C18, C49 and C-54 (recipients)
were infected through units of blood or blood products from donor D36, over a 2-year
period. Long-term follow-up of the six recipients and the donor, shows persistent long
term asymptomatic infection. This group is referred to herein as the long term non-
progressor 1 (LTNP1) cohort. Members of this cohort have been infected for an average
10 of 11 years (10.75 to 14 years) and it was established that the donor had been infected
since April, 1981 (Learmont *et al*, 1992). Regular follow-up includes history, physical
examination, full blood count, T-cell subset counting and measurement of serum p24
antigen and β 2-microglobulin concentrations (Learmont *et al*, 1992; Learmont *et al*,
1995). As controls, sera were obtained from 14 HIV-1 negative individuals (HIV-1-ve),
15 4 patients who were infected with HIV-1 through sexual activity or through blood
transfusion and are also considered long-term non-progressors and 12 HIV-1 positive
(HIV-1+ve) individuals that have developed clinical infections (long term progressors,
LTP). Sera from patients with autoimmune disease and who were HIV-1-ve were also
employed.

20

EXAMPLE 17*Peptide Synthesis*

Peptides corresponding to amino acid residues 1 to 19, 20 to 36, 44 to 65, 72 to 83, 89
to 97, 109 to 114, 121 to 136, 162 to 177, 164 to 186 and 187 to 206 of HIV-1 *nef*
25 (HIV-1_{NL43}) were synthesized using standard t-Boc chemistry and purified by high
pressure chromatography as described elsewhere (Fecondo *et al*, 1993).

EXAMPLE 18*Expression of recombinant HIV-1 Nef protein in E. coli*

30 The large scale expression of the 27 kDa form of HIV-1_{NL43} in *E. coli* and subsequent
purification were as described by Azad *et al* (1994).

EXAMPLE 19

*Screening of sera from HIV-1+ve individuals and control HIV-1-ve groups
for reactivity against Nef protein and derived peptides by direct ELA*

For detecting antibodies that recognise the Nef protein or its peptide derivatives, highly
5 purified full length Nef protein or peptides corresponding to the HIV-1_{NL43} Nef amino
acid sequence were coated onto the wells of 96-well polystyrene microtitre plates at 100
ng/well or 500 ng/well in PBS, respectively. Peptides and proteins were allowed to coat
for 2 h at 37°C. After this incubation period the wells were washed three times with
PBS containing 0.05% v/v Tween 20 (PBS-Tween) and any remaining available sites
10 on the wells blocked by incubation of 150µl of gelatine (1% w/v) in PBS for 1 h at
37°C. Following washing with PBS-Tween as described above, 50µl of serum diluted
in PBS/BSA (1% w/v) was added to the wells and incubated for 1.5 h at 37°C. Sera
added to the wells included that from the seven cohort members (D36, C98, C18, C54,
C49, C64 and C124 [see Learmont *et al*, 1992]) and the control groups described above.
15 The wells were again washed with PBS/Tween and subsequently incubated with 50µl
of biotinylated sheep anti-human Ig (diluted 1:1000 in 1% w/v BSA/PBS; Amersham)
for 1 h at 37°C. Following further washing, 50µl of Streptavidin-HRP (diluted 1:1000
in 1% w/v BSA/PBS; Dakopatts) was added to the wells and the plate incubated at 37°C
for 30 min. An aliquot of 100µl of substrate (0-phenylenediamine, Sigma) was finally
20 added after washing and the plate allowed to incubate at room temperature for 15 min.
The reaction was stopped by the addition of 1 N H₂SO₄ and the plate read at 450/630
nm using a Titertek plate reader.

EXAMPLE 20

25 *Recognition of full length recombinant Nef protein by patient sera*

The prevalence of a Nef-specific antibody response in the cohort members (referred to
herein as (LTNP1), long term progressors (LTP) HIV-1+ve individuals and another
group of long term non-progressors (LTNP2) patients who were infected by different
donors was assessed by EIA. Sera obtained from 14 normal individuals (HIV-1-ve) and
30 14 individuals with autoimmune disease (A/HIV-1-ve) were used as controls.

All individuals who were classified as LTP patients demonstrated high levels of antibodies that recognised full length Nef protein (Figure 12a). Sera obtained from HIV-1-ve or the A/HIV-1-ve groups showed only low level recognition, which was considered at background levels, towards Nef protein (Figure 12b(i)-(iii)). In contrast to normal individuals, sera obtained from the LTNP1 cohort showed high recognition of Nef (Figure 12c), indicating the presence of significant levels of Nef antibodies in the sera of these individuals. The sera titrated out to approximately 1:3000. Similar levels of Nef antibodies were observed in the LTP group (Figure 12a). Nef-positive antibodies were also detected in the LTNP2 group and again titrated at 1:3000 dilution (Figure 12d).

EXAMPLE 21

Recognition of Nef-derived peptides by sera

Recognition of synthetic peptides, which correspond to amino acid sequences of Nef, by the LTNP1 cohort was assessed. Various peptides were assessed to detect those antigenic epitopes of Nef protein recognised by these individuals. Peptides corresponding to amino acid sequences 1 to 19; 20 to 36; 44 to 65; 72 to 83; 89 to 97; 109 to 114; 164 to 186; 187 to 206; 121 to 135 and 162 to 177 of HIV-1_{NL43} Nef protein were used to screen sera for the presence of specific antibodies. All sera from the LTP group recognised all Nef-derived peptides tested (Figure 13a(i)-(x)). Sera titrated between 1:1000 and 1:10,000. Sera from patients with autoimmune disease displayed only low background non-specific recognition. Normal sera from HIV-1-ve individuals tested to date also displayed only background activity (Figure 13b). Sera from the LTNP1 and LTNP2 groups also showed significant reactivity against Nef peptides corresponding to Nef amino acid sequences 1-19, 20-36, 44-65, 72-83, 89-97, 109-114, 121-135, 164-86 and 187-206 (Figure 13c(i)-(x) and d(i)-(x)). Sera from the LTNP2 group also showed significant reactivity against Nef peptide 162-177 (Figure 13d(i)-(x)), similar to that showed by the LTP group, indicating that this region of Nef was immunogenic. However, sera from the LTNP1 cohort showed no significant reactivity towards peptide 162-177 above background levels obtained with normal HIV-1-ve sera (Figure 13c(i)-(x)), indicating that this group of individuals were exposed to cells expressing a Nef protein which did not contain this region. While sera from the

LTNP1 cohort did not react with the peptide corresponding to amino acid residues 162-177 of Nef, the sera from all patients did recognise a longer peptide, 164 to 186, which encompassed most of Nef 162-177. This clearly indicates that the sera recognised antigenic epitopes between 177-186.

5

These results clearly indicate that all individuals from the LNTPI cohort were exposed at some time to HIV-1 infected cells expressing a Nef protein that only had a small deletion encompassing amino acids 162 to 177.

- 10 The antibody testing has identified an antigenic region in the Nef protein which if deleted gives rise to attenuated HIV-1 viral strains. Hence, testing of the HIV-1 positive population may identify further examples of individuals infected with attenuated viral quasispecies. Additionally, lack of recognition of this antigenic epitope offers an antibody assay for testing animals experimentally infected with an HIV-1 *nef* attenuated
- 15 viral strain, in particular deleted in the region covering Nef amino acids 162 to 177 (relative to HIV-1_{NL43} Nef).

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Nicholas J. Deacon
Jennifer C. Learmont
Dale A. McPhee
Suzanne Crowe
David Cooper
- (ii) TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
- (iii) NUMBER OF SEQUENCES: 841
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 - (B) STREET: 400 GARDEN CITY PLAZA
 - (C) CITY: GARDEN CITY
 - (D) STATE: NEW YORK
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 11530-0299
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/477,464
 - (B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PM3864 (AU)
 - (B) FILING DATE: 14-FEB-1994
 - (A) APPLICATION NUMBER: PM4002 (AU)
 - (B) FILING DATE: 21-FEB-1994
 - (A) APPLICATION NUMBER: PN0284 (AU)
 - (B) FILING DATE: 23-DEC-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: FRANK S. DIGIGLIO
 - (C) REFERENCE/DOCKET NUMBER: 9606Z-I
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (516) 742-4343
 - (B) TELEFAX: (516) 742-4366

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGAAGGGCT AATTTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA	60
CACAAGGCTA CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC	120
TGACCTTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA	180
AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG	240
AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTTTCGTAC ATGGCCCGAG	300
AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG	360
CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT	420
GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA	480
GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCCT	540
TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC	600
AGACCCTTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG	660
CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCACGG	720
CAAGAGGCGA GGGGCGGCGA CTGGTGAGTA CGCCAAAAAT TTTGACTAGC GGAGGCTAGA	780
AGGAGAGAGA TGGGTGCGAG AGCGTCGGTA TTAAGCGGGG GAGAATTAGA TAAATGGGAA	840
AAAATTTCGGT TAAGGCCAGG GGGAAAGAAA CAATATAAAC TAAAACATAT AGTATGGGCA	900
AGCAGGGAGC TAGAACGATT CGCAGTTAAT CCTGGCCTTT TAGAGACATC AGAAGGCTGT	960
AGACAAATAC TGGGACAGCT ACAACCATCC CTTCAGACAG GATCAGAAGA ACTTAGATCA	1020
TTATATAATA CAATAGCAGT CCTCTATTGT GTGCATCAAA GGATAGATGT AAAAGACACC	1080
AAGGAAGCCT TAGATAAGAT AGAGGAAGAG CAAAACAAAA GTAAGAAAAA GGCACAGCAA	1140
GCAGCAGCTG ACACAGGAAA CAACAGCCAG GTCAGCCAAA ATTACCCTAT AGTGCAGAAC	1200
CTCCAGGGGC AAATGGTACA TCAGGCCATA TCACCTAGAA CTTTAAATGC ATGGGTAAAA	1260
GTAGTAGAAG AGAAGGCTTT CAGCCCAGAA GTAATACCCA TGTTTTCAGC ATTATCAGAA	1320
GGAGCCACCC CACAAGATTT AAATACCATG CTAAACACAG TGGGGGGACA TCAAGCAGCC	1380
ATGCAAATGT TAAAAGAGAC CATCAATGAG GAAGCTGCAG AATGGGATAG ATTGCATCCA	1440
GTGCATGCAG GGCCTATTGC ACCAGGCCAG ATGAGAGAAC CAAGGGGAAG TGACATAGCA	1500
GGAACACTA GTACCCTTCA GGAACAAATA GGATGGATGA CACATAATCC ACCTATCCCA	1560
GTAGGAGAAA TCTATAAAAG ATGGATAATC CTGGGATTAA ATAAAATAGT AAGAATGTAT	1620
AGCCCTACCA GCATTCTGGA CATAAGACAA GGACCAAAGG AACCCTTTAG AGACTATGTA	1680
GACCGATTCT ATAAAACCTCT AAGAGCCGAG CAAGCTTCAC AAGAGGTAAA AAATTGGATG	1740

ACAGAAACCT	TGTTGGTCCA	AAATGCGAAC	CCAGATTGTA	AGACTATTTT	AAAAGCATTG	1800
GGACCAGGAG	CGACACTAGA	AGAAATGATG	ACAGCATGTC	AGGGAGTGGG	GGGACCCGGC	1860
CATAAAGCAA	GAGTTTTC	TGAAGCAATG	AGCCAAGTAA	CAAATCCAGC	TACCATAATG	1920
ATACAGAAAG	GCAATTTTAG	GAACCAAAGA	AAGACTGTTA	AGTGTTC	TTGTGGCAAA	1980
GAAGGGCACA	TAGCCAAAAA	TTGCAGGGCC	CCTAGGAAAA	AGGGCTGTTG	GAAATGTGGA	2040
AAGGAAGGAC	ACCAAATGAA	AGATTGTACT	GAGAGACAGG	CTAATTTTTT	AGGGAAGATC	2100
TGGCCTTCCC	ACAAGGGAAG	GCCAGGGAAT	TTCTTCAGA	GCAGACCAGA	GCCAACAGCC	2160
CCACCAGAAG	AGAGCTTCAG	GTTTGGGGAA	GAGACAACAA	CTCCCTCTCA	GAAGCAGGAG	2220
CCGATAGACA	AGGAACTGTA	TCCTTTAGCT	TCCCTCAGAT	CACTCTTTGG	CAGCGACCCC	2280
TCGTCACAAT	AAAGATAGGG	GGGCAATTAA	AGGAAGCTCT	ATTAGATACA	GGAGCAGATG	2340
ATACAGTATT	AGAAGAAATG	AATTTGCCAG	GAAGATGGAA	ACCAAAAATG	ATAGGGGGAA	2400
TTGGAGGTTT	TATCAAAGTA	GGACAGTATG	ATCAGATACT	CATAGAAATC	TGCGGACATA	2460
AAGCTATAGG	TACAGTATTA	GTAGGACCTA	CACCTGTCAA	CATAATTGGA	AGAAATCTGT	2520
TGACTCAGAT	TGGCTGCACT	TAAATTTTC	CCATTAGTCC	TATTGAGACT	GTACCAGTAA	2580
AATTAAAGCC	AGGAATGGAT	GGCCAAAAAG	TAAACAATG	GCCATTGACA	GAAGAAAAAA	2640
TAAAAGCATT	AGTAGAAATT	TGTACAGAAA	TGGAAAAGGA	AGGAAAAATT	TCAAAAATTG	2700
GGCCTGAAAA	TCCATACAAT	ACTCCAGTAT	TTGCCATAAA	GA AAAAAGAC	AGTACTAAAT	2760
GGAGAAAATT	AGTAGATTTC	AGAGAACTTA	ATAAGAGAAC	TCAAGATTTC	TGGGAAGTTC	2820
AATTAGGAAT	ACCACATCCT	GCAGGGTTAA	AACAGAAAAA	ATCAGTAACA	GTACTGGATG	2880
TGGGCGATGC	ATATTTTTCA	GTTCCCTTAG	ATAAAGACTT	CAGGAAGTAT	ACTGCATTTA	2940
CCATACCTAG	TATAAAACAAT	GAGACACCAG	GGATTAGATA	TCAGTACAAT	GTGCTTCCAC	3000
AGGGATGGAA	AGGATCACCA	GCAATATTCC	AGTGTAGCAT	GACAAAAATC	TTAGAGCCTT	3060
TTAGAAAACA	AAATCCAGAC	ATAGTCATCT	ATCAATACAT	GGATGATTTG	TATGTAGGAT	3120
CTGACTTAGA	AATAGGGCAG	CATAGAACAA	AAATAGAGGA	ACTGAGACAA	CATCTGTTGA	3180
GGTGGGGATT	TACCACACCA	GACAAAAAAC	ATCAGAAAAG	ACCTCCATTC	CTTTGGATGG	3240
GTTATGAACT	CATCTCTGAT	AAATGGACAG	TACAGCCTAT	AGTGCTGCCA	GAAAAGGACA	3300
GCTGGACTGT	CAATGACATA	CAGAAATTAG	TGGGAAAATT	GAATTGGGCA	AGTCAGATTT	3360
ATGCAGGGAT	TAAAGTAAGG	CAATTATGTA	AACTTCTTAG	GGGAACCAAA	GCACTAACAG	3420
AAGTAGTACC	ACTAACAGAA	GAAGCAGAGC	TAGAACTGGC	AGAAAACAGG	GAGATTCTAA	3480
AAGAACCGGT	ACATGGAGTG	TATTATGACC	CATCAAAAAG	CTTAATAGCA	GAAATACAGA	3540

AGCAGGGGCA	AGGCCAATGG	ACATATCAAA	TTTATCAAGA	GCCATTTAAA	AATCTGAAAA	3600
CAGGAAAATA	TGCAAGAATG	AAGGGTGCCC	ACACTAATGA	TGTGAAACAA	TTAACAGAGG	3660
CAGTACAAAA	AATAGCCACA	GAAAGCATAG	TAATATGGGG	AAAGACTCCT	AAATTTAAAT	3720
TACCCATACA	AAAGGAAACA	TGGGAAGCAT	GGTGGACAGA	GTATTGGCAA	GCCACCTGGA	3780
TTCCTGAGTG	GGAGTTTGTC	AATACCCCTC	CCTTAGTGAA	GTTATGGTAC	CAGTTAGAGA	3840
AAGAACCCAT	AATAGGAGCA	GAAACTTTCT	ATGTAGATGG	GGCAGCCAAT	AGGGAAACTA	3900
AATTAGGAAA	AGCAGGATAT	GTAAC TGACA	GAGGAAGACA	AAAAGTTGTC	CCCCTAACGG	3960
ACACAACAAA	TCAGAAGACT	GAGTTACAAG	CAATTCATCT	AGCTTTGCAG	GATTCGGGAT	4020
TAGAAGTAAA	CATAGTGACA	GA CTCACAAT	ATGCATTGGG	AATCATTCAA	GCACAACCAG	4080
ATAAGAGTGA	ATCAGAGTTA	GTCAGTCAAA	TAATAGAGCA	GTTAATAAAA	AAGGAAAAAG	4140
TCTACCTGGC	ATGGGTACCA	GCACACAAAG	GAATTGGAGG	AAATGAACAA	GTAGATGGGT	4200
TGGTCAGTGC	TGGAATCAGG	AAAGTACTAT	TTTTAGATGG	AATAGATAAG	GCCCAAGAAG	4260
AACATGAGAA	ATATCACAGT	AATTGGAGAG	CAATGGCTAG	TGATTTTAAC	CTACCACCTG	4320
TAGTAGCAAA	AGAAATAGTA	GCCAGCTGTG	ATAAATGTCA	GCTAAAAGGG	GAAGCCATGC	4380
ATGGACAAGT	AGACTGTAGC	CCAGGAATAT	GGCAGCTAGA	TTGTACACAT	TTAGAAGGAA	4440
AAGTTATCTT	GGTAGCAGTT	CATGTAGCCA	GTGGATATAT	AGAAGCAGAA	GTAATTCCAG	4500
CAGAGACAGG	GCAAGAAACA	GCATACTTCC	TCTTAAAATT	AGCAGGAAGA	TGGCCAGTAA	4560
AAACAGTACA	TACAGACAAT	GGCAGCAATT	TCACCAGTAC	TACAGTTAAG	GCCGCCTGTT	4620
GGTGGGCGGG	GATCAAGCAG	GAATTTGGCA	TTCCCTACAA	TCCCCAAAGT	CAAGGAGTAA	4680
TAGAATCTAT	GAATAAAGAA	TTAAAGAAAA	TTATAGGACA	GGTAAGAGAT	CAGGCTGAAC	4740
ATCTTAAGAC	AGCAGTACAA	ATGGCAGTAT	TCATCCACAA	TTTTAAAAGA	AAAGGGGGGA	4800
TTGGGGGGTA	CAGTGCAGGG	GAAAGAATAG	TAGACATAAT	AGCAACAGAC	ATACAAACTA	4860
AAGAATTACA	AAAACAAATT	ACAAAAATTC	AAAATTTTCG	GGTTTATTAC	AGGGACAGCA	4920
GAGATCCAGT	TTGGAAAGGA	CCAGCAAAGC	TCCTCTGGAA	AGGTGAAGGG	GCAGTAGTAA	4980
TACAAGATAA	TAGTGACATA	AAAGTAGTGC	CAAGAAGAAA	AGCAAAGATC	ATCAGGGATT	5040
ATGGAAAACA	GATGGCAGGT	GATGATTGTG	TGGCAAGTAG	ACAGGATGAG	GATTAACACA	5100
TGGAAGAGAT	TAGTAAAACA	CCATATGTAT	ATTTCAAGGA	AAGCTAAGGA	CTGGTTTTAT	5160
AGACATCACT	ATGAAAGTAC	TAATCCAAAA	ATAAGTTCAG	AAGTACACAT	CCCCTAGGGG	5220
GATGCTAAAT	TAGTAATAAC	AACATATTGG	GGTCTGCATA	CAGGAGAAAG	AGACTGGCAT	5280
TTGGGTCAGG	GAGTCTCCAT	AGAATGGAGG	AAAAAGAGAT	ATAGCACACA	AGTAGACCCCT	5340

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GACCTAGCAG	ACCAACTAAT	TCATCTGCAC	TATTTTGATT	GTTTTTCAGA	ATCTGCTATA	5400
AGAAATACCA	TATTAGGACG	TATAGTTAGT	CCTAGGTGTG	AATATCAAGC	AGGACATAAC	5460
AAGGTAGGAT	CTCTACAGTA	CTTGGCACTA	GCAGCATTAA	TAAAACCAAA	ACAGATAAAG	5520
CCACCTTTGC	CTAGTGTTAG	GAAACTGACA	GAGGACAGAT	GGAACAAGCC	CCAGAAGACC	5580
AAGGGCCACA	GAGGGAGCCA	TACAATGAAT	GGACACTAGA	GCTTTTAGAG	GAACCTAAGA	5640
GTGAAGCTGT	TAGACATTTT	CCTAGGATAT	GGCTCCATAA	CTTAGGACAA	CATATCTATG	5700
AAACTTACGG	GGATACTTGG	GCAGGAGTGG	AAGCCATAAT	AAGAATTCTG	CAACAACCTGC	5760
TGTTTATCCA	TTTCAGAATT	GGTGTCGAC	ATAGCAGAAT	AGGCGTACT	CGACAGAGGA	5820
GAGCAAGAAA	TGGAGCCAGT	AGATCCTAGA	CTAGAGCCCT	GGAAGCATCC	AGGAAGTCAG	5880
CCTAAAACCTG	CTTGTAACCA	TTGCTATTGT	AAAAAGTGTT	GCTTTCATTG	CCAAGTTTGT	5940
TTCATGACAA	AAGCCTTAGG	CATCTCCTAT	GGCAGGAAGA	AGCGGAGACA	GCGACGAAGA	6000
GCTCATCAGA	ACAGTCAGAC	TCATCAAGCT	TCTCTATCAA	AGCAGTAAGT	AGTACATGTA	6060
ATGCAACCTA	TAATAGTAGC	AATAGTAGCA	TTAGTAGTAG	CAATAATAAT	AGCAATAGTT	6120
GTGTGGTCCA	TAGTAATCAT	AGAATATAGG	AAAATATTAA	GACAAAGAAA	AATAGACAGG	6180
TTAATTGATA	GACTAATAGA	AAGAGCAGAA	GACAGTGGCA	ATGAGAGTGA	AGGAGAAGTA	6240
TCAGCACTTG	TGGAGATGGG	GGTGGAATG	GGGCACCATG	CTCCTTGGA	TATTGATGAT	6300
CTGTAGTGCT	ACAGAAAAAT	TGTGGGTCAC	AGTCTATTAT	GGGGTACCTG	TGTGGAAGGA	6360
AGCAACCACC	ACTCTATTTT	GTGCATCAGA	TGCTAAAGCA	TATGATACAG	AGGTACATAA	6420
TGTTTGGGCC	ACACATGCCT	GTGTACCCAC	AGACCCCAAC	CCACAAGAAG	TAGTATTGGT	6480
AAATGTGACA	GAAAATTTTA	ACATGTGGAA	AAATGACATG	GTAGAACAGA	TGCATGAGGA	6540
TATAATCAGT	TTATGGGATC	AAAGCCTAAA	GCCATGTGTA	AAATTAACCC	CACTCTGTGT	6600
TAGTTTAAAG	TGCACTGATT	TGAAGAATGA	TACTAATACC	AATAGTAGTA	GCGGGAGAAT	6660
GATAATGGAG	AAAGGAGAGA	TAAAAAACTG	CTCTTTCAAT	ATCAGCACAA	GCATAAGAGA	6720
TAAGGTGCAG	AAAGAATATG	CATTCTTTTA	TAAACTTGAT	ATAGTACCAA	TAGATAATAC	6780
CAGCTATAGG	TTGATAAGTT	GTAACACCTC	AGTCATTACA	CAGGCCTGTC	CAAAGGTATC	6840
CTTTGAGCCA	ATTCCCATAC	ATTATTGTGC	CCCGGCTGGT	TTTGCGATTC	TAAAATGTAA	6900
TAATAAGACG	TTCAATGGAA	CAGGACCATG	TACAAATGTC	AGCACAGTAC	AATGTACACA	6960
TGGAATCAGG	CCAGTAGTAT	CAACTCAACT	GCTGTTAAAT	GGCAGTCTAG	CAGAAGAAGA	7020
TGTAGTAATT	AGATCTGCCA	ATTTACAGAG	CAATGCTAAA	ACCATAATAG	TACAGCTGAA	7080
CACATCTGTA	GAAATTAATT	GTACAAGACC	CAACAACAAT	ACAAGAAAAA	GTATCCGTAT	7140

CCAGAGGGGA	CCAGGGAGAG	CATTTGTTAC	AATAGGAAAA	ATAGGAAATA	TGAGACAAGC	7200
ACATTGTAAC	ATTAGTAGAG	CAAAATGGAA	TGCCACTTTA	AAACAGATAG	CTAGCAAATT	7260
AAGAGAACAA	TTTGAAATA	ATAAAACAAT	AATCTTTAAG	CAATCCTCAG	GAGGGGACCC	7320
AGAAATTGTA	ACGCACAGTT	TTAATTGTGG	AGGGGAATTT	TTCTACTGTA	ATTCAACACA	7380
ACTGTTTAAT	AGTACTTGGT	TTAATAGTAC	TTGGAGTACT	GAAGGGTCAA	ATAACACTGA	7440
AGGAAGTGAC	ACAATCACAC	TCCCATGCAG	AATAAAACAA	TTTATAAACA	TGTGGCAGGA	7500
AGTAGGAAAA	GCAATGTATG	CCCCTCCCAT	CAGTGGACAA	ATTAGATGTT	CATCAAATAT	7560
TACTGGGCTG	CTATTAACAA	GAGATGGTGG	TAATAACAAC	AATGGGTCCG	AGATCTTCAG	7620
ACCTGGAGGA	GGCGATATGA	GGGACAATTG	GAGAAGTGAA	TTATATAAAT	ATAAAGTAGT	7680
AAAAATTGAA	CCATTAGGAG	TAGCACCCAC	CAAGGCAAAG	AGAAGAGTGG	TGCAGAGAGA	7740
AAAAAGAGCA	GTGGGAATAG	GAGCTTTGTT	CCTTGGGTTC	TTGGGAGCAG	CAGGAAGCAC	7800
TATGGGCTGC	ACGTCAATGA	CGCTGACGGT	ACAGGCCAGA	CAATTATTGT	CTGATATAGT	7860
GCAGCAGCAG	AACAATTTGC	TGAGGGCTAT	TGAGGCCGAA	CAGCATCTGT	TGCAACTCAC	7920
AGTCTGGGGC	ATCAAAACAGC	TCCAGGCAAG	AATCCTGGCT	GTGGAAAGAT	ACCTAAAGGA	7980
TCAACAGCTC	CTGGGGATTT	GGGGTTGCTC	TGGAAACTC	ATTTGCACCA	CTGCTGTGCC	8040
TTGGAATGCT	AGTTGGAGTA	ATAAATCTCT	GGAACAGATT	TGGAATAACA	TGACCTGGAT	8100
GGAGTGGGAC	AGAGAAATTA	ACAATTACAC	AAGCTTAATA	CACTCCTTAA	TTGAAGAATC	8160
GCAAAACCAG	CAAGAAAAGA	ATGAACAAGA	ATTATTGGAA	TTAGATAAAT	GGGCAAGTTT	8220
GTGGAATTGG	TTTAACATAA	CAAATTGGCT	GTGGTATATA	AAATTATTCA	TAATGATAGT	8280
AGGAGGCTTG	GTAGGTTTAA	GAATAGTTTT	TGCTGTACTT	TCTATAGTGA	ATAGAGTTAG	8340
GCAGGGATAT	TCACCATTAT	CGTTTCAGAC	CCACCTCCCA	ATCCCAGGGG	GACCCGACAG	8400
GCCCCAAGGA	ATAGAAGAAG	AAGGTGGAGA	GAGAGACAGA	GACAGATCCA	TTCGATTAGT	8460
GAACGGATCC	TTAGCACTTA	TCTGGGACGA	TCTGCGGAGC	CTGTGCCTCT	TCAGCTACCA	8520
CCGCTTGAGA	GACTTACTCT	TGATTGTAAC	GAGGATTGTG	GAACTTCTGG	GACGCAGGGG	8580
GTGGGAAGCC	CTCAAATATT	GGTGAATCT	CCTACAGTAT	TGGAGTCAGG	AACTAAAGAA	8640
TAGTGCTGTT	AACTTGCTCA	ATGCCACAGC	CATAGCAGTA	GCTGAGGGGA	CAGATAGGGT	8700
TATAGAAGTA	TTACAAGCAG	CTTATAGAGC	TATTGCCAC	ATACCTAGAA	GAATAAGACA	8760
GGGCTTGGA	AGGATTTTGC	TATAAGATGG	GTGGCAAGTG	GTCAAAAAGT	AGTGTGATTG	8820
GATGGCCTGC	TGTAAGGGAA	AGAATGAGAC	GAGCTGAGCC	AGCAGCAGAT	GGGGTGGGAG	8880
CAGTATCTCG	AGACCTAGAA	AAACATGGAG	CAATCACAAG	TAGCAATACA	GCAGCTAACA	8940

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ATGCTGCTTG	TGCCTGGCTA	GAAGCACAAG	AGGAGGAAGA	GGTGGGTTTT	CCAGTCACAC	9000
CTCAGGTACC	TTTAAGACCA	ATGACTTACA	AGGCAGCTGT	AGATCTTAGC	CACTTTTTTAA	9060
AAGAAAAGGG	GGGACTGGAA	GGGCTAATTC	ACTCCCAAAG	AAGACAAGAT	ATCCTTGATC	9120
TGTGGATCTA	CCACACACAA	GGCTACTTCC	CTGATTGGCA	GAACTACACA	CCAGGGCCAG	9180
GGGTCAGATA	TCCACTGACC	TTTGGATGGT	GCTACAAGCT	AGTACCAGTT	GAGCCAGATA	9240
AGGTAGAAGA	GGCCAATAAA	GGAGAGAACA	CCAGCTTGTT	ACACCCTGTG	AGCCTGCATG	9300
GAATGGATGA	CCCTGAGAGA	GAAGTGTTAG	AGTGGAGGTT	TGACAGCCGC	CTAGCATTTT	9360
ATCACGTGGC	CCGAGAGCTG	CATCCGGAGT	ACTTCAAGAA	CTGCTGACAT	CGAGCTTGCT	9420
ACAAGGGACT	TTCCGCTGGG	GACTTTCCAG	GGAGGCGTGG	CCTGGGCGGG	ACTGGGGAGT	9480
GGCGAGCCCT	CAGATGCTGC	ATATAAGCAG	CTGCTTTTTG	CCTGTACTGG	GTCTCTCTGG	9540
TTAGACCAGA	TCTGAGCCTG	GGAGCTCTCT	GGCTAACTAG	GGAACCCACT	GCTTAAGCCT	9600
CAATAAAGCT	TGCCTTGAGT	GCTTCAAGTA	GTGTGTGCCC	GTCTGTTGTG	TGACTCTGGT	9660
AACTAGAGAT	CCCTCAGACC	CTTTTAGTCA	GTGTGGAAAA	TCTCTAGCA		9709

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGTGGCA

10

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGGGTGGCAA

10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGTGGCAAG

10

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGGCAAGT

10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGGCAAGTG

10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGGCAAGTGG

10

(2) INFORMATION FOR SEQ ID NO:8:

0914573.00353

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAAGTGGT

10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAAGTGGTC

10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAAGTGGTCA

10

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGTGGTCAA

10

(2) INFORMATION FOR SEQ ID NO:12:

001453, 000393

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTGGTCAAA

10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTGGTCAAAA

10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGGTCAAAAA

10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTCAAAAAG

10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCAAAAAGT

10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCAAAAAGTA

10

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAAAAAGTAG

10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAAAAAGTAGT

10

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAAAGTAGTG

10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAAGTAGTGT

10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGTAGTGTG

10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGTAGTGTGA

10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTAGTGTGAT

10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAGTGTGATT

10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGTGTGATTG

10

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGTGATTGG

10

(2) INFORMATION FOR SEQ ID NO:28:

000000-000000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGTGATTGGA

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGATTGGAT

10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGATTGGATG

10

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATTGGATGG

10

(2) INFORMATION FOR SEQ ID NO:32:

0914673.00099

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTGGATGGC

10

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTGGATGGCC

10

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGGATGGCCT

10

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGATGGCCTG

10

(2) INFORMATION FOR SEQ ID NO:36:

09145783 100396

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GATGGCCTGC

10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGCCTGCT

10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGCCTGCTG

10

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCCTGCTGT

10

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCCTGCTGTA

10

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCTGCTGTAA

10

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTGCTGTAAG

10

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCTGTAAGG

10

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTGTAAGGG

10

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGTAAGGGA

10

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGTAAGGGAA

10

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTAAGGGAAA

10

(2) INFORMATION FOR SEQ ID NO:48:

001463-09390

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TAAGGGAAAG

10

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAGGGAAAGA

10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGGGAAAGAA

10

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGGAAAGAAT

10

(2) INFORMATION FOR SEQ ID NO:52:

094457-09036

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGAAAGAATG

10

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAAGAATGA

10

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AAAGAATGAG

10

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AAGAATGAGA

10

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGAATGAGAC

10

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATGAGACG

10

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AATGAGACGA

10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGAGACGAG

10

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGAGACGAGC

10

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAGACGAGCT .

10

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGACGAGCTG

10

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GACGAGCTGA

10

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACGAGCTGAG

10

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGAGCTGAGC

10

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAGCTGAGCC

10

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AGCTGAGCCA

10

(2) INFORMATION FOR SEQ ID NO:68:

004467-09090
000000-000000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTGAGCCAG

10

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGAGCCAGC

10

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TGAGCCAGCA

10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAGCCAGCAG

10

(2) INFORMATION FOR SEQ ID NO:72:

00446703-090300

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AGCCAGCAGC

10

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCCAGCAGCA

10

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCAGCAGCAG

10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAGCAGCAGA

10

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AGCAGCAGAT

10

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCAGCAGATG

10

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGCAGATGG

10

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCAGATGGG

10

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCAGATGGGG

10

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CAGATGGGGT

10

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGATGGGGTG

10

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATGGGGTGG

10

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGGGGTGGG

10

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGGGGTGGGA

10

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGGGTGGGAG

10

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGGTGGGAGC

10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGTGGGAGCA

10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGGAGCAG

10

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGGAGCAGT

10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGGAGCAGTA

10

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGAGCAGTAT

10

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAGCAGTATC

10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGCAGTATCT

10

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GCAGTATCTC

10

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGTATCTCG

10

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGTATCTCGA

10

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTATCTCGAG

10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TATCTCGAGA

10

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATCTCGAGAC

10

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTCGAGACC

10

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTCGAGACCT

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TCGAGACCTA

10

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGAGACCTAG

10

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAGACCTAGA

10

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGACCTAGAA

10

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GACCTAGAAA

10

(2) INFORMATION FOR SEQ ID NO:108:

0044394160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ACCTAGAAAA

10

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCTAGAAAAA

10

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTAGAAAAAC

10

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TAGAAAAACA

10

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AGAAAAACAT

10

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAAAAACATG

10

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AAAAACATGG

10

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

AAAACATGGA

10

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

AAACATGGAG

10

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AACATGGAGC

10

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACATGGAGCA

10

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CATGGAGCAA

10

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATGGAGCAAT

10

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGAGCAATC

10

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGAGCAATCA

10

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAGCAATCAC

10

(2) INFORMATION FOR SEQ ID NO:124:

091457B-0038
B6E060-EB294160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

AGCAATCACA

10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCAATCACAA

10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAATCACAAG

10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AATCACAAGT

10

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ATCACAAGTA

10

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TCACAAGTAG

10

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CACAAGTAGC

10

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ACAAGTAGCA

10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CAAGTAGCAA

10

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAGTAGCAAT

10

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

AGTAGCAATA

10

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GTAACAATAC

10

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TAGCAATACA

10

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AGCAATACAG

10

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAATACAGC

10

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CAATACAGCA

10

(2) INFORMATION FOR SEQ ID NO:140:

094163, 090360
"EB294T60"

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

AATACAGCAG

10

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ATACAGCAGC

10

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TACAGCAGCT

10

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACAGCAGCTA

10

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CAGCAGCTAA

10

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCAGCTAAC

10

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGCTAACA

10

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CAGCTAACAA

10

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AGCTAACAAT

10

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GCTAACAATG

10

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CTAACAATGC

10

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TAACAATGCT

10

(2) INFORMATION FOR SEQ ID NO:152:

00462-0930

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

AACAATGCTG

10

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAATGCTGC

10

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CAATGCTGCT

10

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

AATGCTGCTT

10

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ATGCTGCTTG

10

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TGCTGCTTGT .

10

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCTGCTTGTG

10

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CTGCTTGTGC

10

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TGCTTGTGCC

10

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GCTTGTGCCT

10

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CTTGTGCCTG

10

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

TTGTGCCTGG

10

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTGCCTGGC

10

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTGCCTGGCT

10

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TGCCTGGCTA

10

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GCCTGGCTAG

10

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CCTGGCTAGA

10

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTGGCTAGAA

10

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TGGCTAGAAG

10

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCTAGAAGC

10

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GCTAGAAGCA

10

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTAGAAGCAC

10

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TAGAAGCACA

10

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGAAGCACAA

10

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAGCACAAG

10

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AAGCACAAGA

10

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AGCACAAGAG

10

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCACAAGAGG

10

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CACAAGAGGA

10

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ACAAGAGGAG

10

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CAAGAGGAGG

10

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AAGAGGAGGA

10

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

AGAGGAGGAA

10

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAGGAGGAAG

10

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

AGGAGGAAGA

10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GGAGGAAGAG

10

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAGGAAGAGG

10

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

AGGAAGAGGT

10

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGAAGAGGTG

10

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAAGAGGTGG

10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

AAGAGGTGGG

10

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

AGAGGTGGGT

10

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAGGTGGGTT

10

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AGGTGGGTTT

10

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTGGGTTTT

10

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GTGGGTTTTC

10

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TGGGTTTTC

10

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GGGTTTCCA

10

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGTTTTCCAG

10

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GTTTCCAGT

10

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTCCAGTC

10

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTCCAGTCA

10

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTCCAGTCAC

10

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TCCAGTCACA

10

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCAGTCACAC

10

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CAGTCACACC

10

(2) INFORMATION FOR SEQ ID NO:208:

00145703.000300

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGTCACACCT

10

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GTCACACCTC

10

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

TCACACCTCA

10

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CACACCTCAG

10

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACACCTCAGG

10

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CACCTCAGGT

10

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCTCAGGTA

10

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CCTCAGGTAC

10

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCAGGTACC

10

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TCAGGTACCT

10

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CAGGTACCTT

10

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

AGGTACCTTT

10

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGTACCTTTA 10

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GTACCTTTAA 10

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TACCTTTAAG 10

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ACCTTTAAGA 10

(2) INFORMATION FOR SEQ ID NO:224:

00146783-090398

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CCTTTAAGAC

10

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CTTTAAGACC

10

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTTAAGACCA

10

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TTAAGACCAA

10

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TAAGACCAAT

10

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AAGACCAATG

10

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

AGACCAATGA

10

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GACCAATGAC

10

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ACCAATGACT

10

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CCAATGACTT

10

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CAATGACTTA

10

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AATGACTTAC

10

(2) INFORMATION FOR SEQ ID NO:236:

(ii) MOLECULE TYPE: DNA

ATGACTTACA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TGACTTACAA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GACTTACAAG

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

ACTTACAAGG

10

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CTTACAAGGC

10

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TTACAAGGCA

10

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TACAAGGCAG

10

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ACAAGGCAGC

10

(2) INFORMATION FOR SEQ ID NO:244:

00443-EB29460

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CAAGGCAGCT

10

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

AAGGCAGCTG

10

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

AGGCAGCTGT

10

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GGCAGCTGTA

10

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GCAGCTGTAG

10

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

CAGCTGTAGA

10

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

AGCTGTAGAT

10

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GCTGTAGATC

10

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CTGTAGATCT

10

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TGTAGATCTT

10

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

G TAGATCTTA

10

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TAGATCTTAG

10

(2) INFORMATION FOR SEQ ID NO:256:

09446733-000209

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

AGATCTTAGC

10

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GATCTTAGCC

10

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

ATCTTAGCCA

10

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TCTTAGCCAC

10

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CTTAGCCACT

10

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TTAGCCACTT

10

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TAGCCACTTT

10

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

AGCCACTTTT

10

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GCCACTTTTT

10

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

CCACTTTTTTA

10

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CACTTTTTTAA

10

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ACTTTTTTAAA

10

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CTTTTAAAA

10

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTTTTAAAAG

10

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TTTTAAAAGA

10

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TTTAAAAGAA

10

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTAAAAGAAA

10

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TAAAAGAAAA

10

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

AAAAGAAAAG

10

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

AAAGAAAAGG

10

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGAAAAGGG

10

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

AGAAAAGGGG

10

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAAAAGGGGG

10

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

AAAAGGGGGG

10

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

AAAGGGGGGA

10

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

AAGGGGGGAC

10

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

AGGGGGGACT

10

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GGGGGGGACTG

10

(2) INFORMATION FOR SEQ ID NO:284:

(ii) MOLECULE TYPE: DNA

GGGGGACTGG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GGGGACTGGA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GGGACTGGAA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

GGACTGGAAG

10

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GACTGGAAGG

10

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ACTGGAAGGG

10

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CTGGAAGGGC

10

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TGGAAGGGCT

10

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GGAAGGGCTA

10

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAAGGGCTAA

10

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

AAGGGCTAAT

10

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

AGGGCTAATT

10

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GGGCTAATTC

10

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GGCTAATTCA

10

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GCTAATTCAC

10

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

CTAATTCACT

10

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

TAATTCATC

10

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AATTCATCC

10

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

ATTCATCCC

10

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TTCACTCCCA

10

(2) INFORMATION FOR SEQ ID NO:304:

001463-EBZGHT60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

TCACTCCCAA

10

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CACTCCCAAA

10

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

ACTCCCAAAG

10

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

CTCCCAAAGA

10

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

TCCCAAAGAA

10

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

CCCAAAGAAG

10

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

CCAAAGAAGA

10

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CAAAGAAGAC

10

(2) INFORMATION FOR SEQ ID NO:312:

20250323 14:54:00

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AAAGAAGACA

10

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AAGAAGACAA

10

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AGAAGACAAG

10

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAAGACAAGA

10

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AAGACAAGAT

10

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AGACAAGATA

10

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GACAAGATAT

10

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ACAAGATATC

10

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

CAAGATATCC

10

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AAGATATCCT

10

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AGATATCCTT

10

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GATATCCTTG

10

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

ATATCCTTGA

10

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

TATCCTTGAT

10

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

ATCCTTGATC

10

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

TCCTTGATCT

10

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CCTTGATCTG

10

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

CTTGATCTGT

10

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

TTGATCTGTG

10

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

TGATCTGTGG

10

(2) INFORMATION FOR SEQ ID NO:332:

00446793-090399

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GATCTGTGGA

10

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

ATCTGTGGAT

10

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

TCTGTGGATC

10

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

CTGTGGATCT

10

(2) INFORMATION FOR SEQ ID NO:336:

004463-09090

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

TGTGGATCTA

10

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GTGGATCTAC

10

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

TGGATCTACC

10

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GGATCTACCA

10

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GATCTACCAC

10

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

ATCTACCACA

10

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TCTACCACAC

10

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CTACCACACA

10

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

TACCACACAC

10

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ACCACACACA

10

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

CCACACACAA

10

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

CACACACAAG

10

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ACACACAAGG

10

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

CACACAAGGC

10

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

ACACAAGGCT

10

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

CACAAGGCTA

10

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ACAAGGCTAC

10

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CAAGGCTACT

10

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

AAGGCTACTT

10

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

AGGCTACTTC

10

(2) INFORMATION FOR SEQ ID NO:356:

00446-EBZ94T60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GGCTACTTCC

10

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCTACTTCCC

10

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CTACTTCCCT

10

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

TACTTCCCTG

10

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

ACTTCCCTGA

10

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

CTTCCCTGAT

10

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

TTCCCTGATT

10

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCCCTGATTG

10

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

CCCTGATTGG

10

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

CCTGATTGGC

10

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

CTGATTGGCA

10

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

TGATTGGCAG

10

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GATTGGCAGA

10

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

ATTGGCAGAA

10

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

TTGGCAGAAC

10

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

TGGCAGAACT

10

(2) INFORMATION FOR SEQ ID NO:372:

00446788-000368

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GGCAGAACTA

10

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GCAGAACTAC

10

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

CAGAACTACA

10

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

AGAACTACAC

10

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GAACTACACA

10

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

AACTACACAC

10

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

ACTACACACC

10

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

CTACACACCA

10

(2) INFORMATION FOR SEQ ID NO:380:

004463-09098
"EE050" E8/94T60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

TACACACCAG 10

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

ACACACCAGG 10

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CACACCAGGG 10

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ACACCAGGGC 10

(2) INFORMATION FOR SEQ ID NO:384:

004463.09039

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

CACCAGGGCC

10

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

ACCAGGGCCA

10

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CCAGGGCCAG

10

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

CAGGGCCAGG

10

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

AGGGCCAGGG

10

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGGCCAGGGG

10

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GGCCAGGGGT

10

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GCCAGGGGTC

10

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

CCAGGGGTCA

10

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

CAGGGGTCAG

10

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

AGGGGTCAGA

10

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GGGGTCAGAT

10

(2) INFORMATION FOR SEQ ID NO:396:

001463-090396

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GGGTCAGATA

10

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GGTCAGATAT

10

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GTCAGATATC

10

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TCAGATATCC

10

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

CAGATATCCA

10

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

AGATATCCAC

10

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GATATCCACT

10

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

ATATCCACTG

10

(2) INFORMATION FOR SEQ ID NO:404:

(ii) MOLECULE TYPE: DNA

TATCCACTGA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

ATCCACTGAC

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TCCACTGACC

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

CCACTGACCT

10

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

CACTGACCTT

10

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

ACTGACCTTT

10

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTGACCTTTG

10

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

TGACCTTTGG

10

(2) INFORMATION FOR SEQ ID NO:412:

(ii) MOLECULE TYPE: DNA

GACCTTTGGA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

ACCTTTGGAT

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CCTTTGGATG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

CTTTGGATGG

10

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

TTGGATGGT

10

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

TTGGATGGTG .

10

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGGATGGTGC

10

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GGATGGTGCT

10

(2) INFORMATION FOR SEQ ID NO:420:

00446783-090393

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GATGGTGCTA

10

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

ATGGTGCTAC

10

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

TGGTGCTACA

10

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GGTGCTACAA

10

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GTGCTACAAG

10

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

TGCTACAAGC

10

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCTACAAGCT

10

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

CTACAAGCTA

10

(2) INFORMATION FOR SEQ ID NO:428:

004457-09098
000000-000000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

TACAAGCTAG

10

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

ACAAGCTAGT

10

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

CAAGCTAGTA

10

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

AAGCTAGTAC

10

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

AGCTAGTACC

10

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GCTAGTACCA

10

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

CTAGTACCAG

10

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

TAGTACCAGT

10

(2) INFORMATION FOR SEQ ID NO:436:

004462-090390

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

AGTACCAGTT

10

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GTACCAGTTG

10

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

TACCAGTTGA

10

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

ACCAGTTGAG

10

(2) INFORMATION FOR SEQ ID NO:440:

BB3059 EB294T60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

CCAGTTGAGC

10

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

CAGTTGAGCC

10

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

AGTTGAGCCA

10

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GTTGAGCCAG

10

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

TTGAGCCAGA

10

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

TGAGCCAGAT

10

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GAGCCAGATA

10

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

AGCCAGATAA

10

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GCCAGATAAG

10

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CCAGATAAGG

10

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CAGATAAGGT

10

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

AGATAAGGTA

10

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GATAAGGTAG

10

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

ATAAGGTAGA

10

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

TAAGGTAGAA

10

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AAGGTAGAAG

10

(2) INFORMATION FOR SEQ ID NO:456:

001463 090399

(ii) MOLECULE TYPE: DNA

AGGTAGAAGA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GGTAGAAGAG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GTAGAAGAGG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

TAGAAGAGGC

10

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

AGAAGAGGCC

10

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAAGAGGCCA

10

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

AAGAGGCCAA

10

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

AGAGGCCAAT

10

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAGGCCAATA

10

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

AGGCCAATAA

10

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGCCAATAAA

10

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GCCAATAAAG

10

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CCAATAAAGG

10

(2) INFORMATION FOR SEQ ID NO:469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CAATAAAGGA

10

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

AATAAAGGAG

10

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

ATAAAGGAGA

10

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

TAAAGGAGAG

10

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

AAAGGAGAGA

10

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

AAGGAGAGAA

10

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

AGGAGAGAAC

10

(2) INFORMATION FOR SEQ ID NO:476:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GGAGAGAACA

10

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAGAGAACAC

10

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

AGAGAACACC

10

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAGAACACCA

10

(2) INFORMATION FOR SEQ ID NO:480:

(ii) MOLECULE TYPE: DNA

AGAACACCAG

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAACACCAGC

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

AACACCAGCT

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

ACACCAGCTT

10

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

CACCAGCTTG

10

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

ACCAGCTTGT

10

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

CCAGCTTGTT

10

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

CAGCTTGTTA

10

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

AGCTTGTTAC

10

(2) INFORMATION FOR SEQ ID NO:489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GCTTGTTACA

10

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

CTTGTTACAC

10

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

TTGTACACC

10

(2) INFORMATION FOR SEQ ID NO:492:

09442-0039

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

TGTTACACCC

10

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GTTACACCCT

10

(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TTACACCCTG

10

(2) INFORMATION FOR SEQ ID NO:495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

TACACCCTGT

10

(2) INFORMATION FOR SEQ ID NO:496:

BBE000"EBL947ED

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

ACACCCTGTG

10

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

CACCCTGTGA

10

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

ACCCTGTGAG

10

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

CCCTGTGAGC

10

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

CCTGTGAGCC

10

(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

CTGTGAGCCT

10

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TGTGAGCCTG

10

(2) INFORMATION FOR SEQ ID NO:503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GTGAGCCTGC

10

(2) INFORMATION FOR SEQ ID NO:504:

00443 00393

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

TGAGCCTGCA

10

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAGCCTGCAT

10

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

AGCCTGCATG

10

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GCCTGCATGG

10

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

CCTGCATGGA

10

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTGCATGGAA

10

(2) INFORMATION FOR SEQ ID NO:510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

TGCATGGAAT

10

(2) INFORMATION FOR SEQ ID NO:511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GCATGGAATG

10

(2) INFORMATION FOR SEQ ID NO:512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

CATGGAATGG

10

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

ATGGAATGGA

10

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

TGGAATGGAT

10

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGAATGGATG

10

(2) INFORMATION FOR SEQ ID NO:516:

0044594760

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAATGGATGA

10

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

AATGGATGAC

10

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

ATGGATGACC

10

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

TGGATGACCC

10

(2) INFORMATION FOR SEQ ID NO:520:

001463-090358
85E069 E8294160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GGATGACCCT

10

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GATGACCCTG

10

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

ATGACCCTGA

10

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

TGACCCTGAG

10

(2) INFORMATION FOR SEQ ID NO:524:

20250709 14:50:45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GACCCTGAGA

10

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

ACCCTGAGAG

10

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

CCCTGAGAGA

10

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

CCTGAGAGAG

10

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

CTGAGAGAGA

10

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

TGAGAGAGAA

10

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GAGAGAGAAG

10

(2) INFORMATION FOR SEQ ID NO:531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

AGAGAGAAGT

10

(2) INFORMATION FOR SEQ ID NO:532:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAGAGAAGTG

10

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

AGAGAAGTGT

10

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GAGAAGTGTT

10

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

AGAAGTGTTA

10

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAAGTGTTAG

10

(2) INFORMATION FOR SEQ ID NO:537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

AAGTGTTAGA

10

(2) INFORMATION FOR SEQ ID NO:538:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

AGTGTTAGAG

10

(2) INFORMATION FOR SEQ ID NO:539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GTGTTAGAGT

10

(2) INFORMATION FOR SEQ ID NO:540:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

TGTTAGAGTG

10

(2) INFORMATION FOR SEQ ID NO:541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GTTAGAGTGG

10

(2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

TTAGAGTGGA

10

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

TAGAGTGGAG

10

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

AGAGTGGAGG

10

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAGTGGAGGT

10

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

AGTGGAGGTT

10

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GTGGAGGTTT

10

(2) INFORMATION FOR SEQ ID NO:548:

55E060"EE294T60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

TGGAGGTTTG

10

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGAGGTTTGA

10

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GAGGTTTGAC

10

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

AGGTTTGACA

10

(2) INFORMATION FOR SEQ ID NO:552:

00146783-090396

(ii) MOLECULE TYPE: DNA

GGTTTGACAG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:553:

GTTTGACAGC

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TTTGACAGCC

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TTGACAGCCG

10

(2) INFORMATION FOR SEQ ID NO:556:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

TGACAGCCGC

10

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GACAGCCGCC

10

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

ACAGCCGCCT

10

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

CAGCCGCCTA

10

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

AGCCGCCTAG

10

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GCCGCCTAGC

10

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

CCGCCTAGCA

10

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

CGCCTAGCAT

10

(2) INFORMATION FOR SEQ ID NO:564:

00446783-090393

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GCCTAGCATT

10

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

CCTAGCATTT

10

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

CTAGCATTTTC

10

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TAGCATTTCA

10

(2) INFORMATION FOR SEQ ID NO:568:

(ii) MOLECULE TYPE: DNA

AGCATTTCAT

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GCATTTCATC

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

CATTTCATCA

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

ATTTCATCAC

10

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

TTTCATCACG

10

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

TTCATCACGT

10

(2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

TCATCACGTG

10

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CATCACGTGG

10

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

ATCACGTGGC

10

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

TCACGTGGCC

10

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

CACGTGGCCC

10

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

ACGTGGCCCC

10

(2) INFORMATION FOR SEQ ID NO:580:

0014673-00393

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

CGTGGCCCGA

10

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GTGGCCCGAG

10

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

TGGCCCGAGA

10

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCCCGAGAG

10

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GCCCGAGAGC

10

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

CCCGAGAGCT

10

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

CCGAGAGCTG

10

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

CGAGAGCTGC

10

(2) INFORMATION FOR SEQ ID NO:588:

094163 090969

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAGAGCTGCA

10

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

AGAGCTGCAT

10

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAGCTGCATC

10

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

AGCTGCATCC

10

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GCTGCATCCG

10

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CTGCATCCGG

10

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

TGCATCCGGA

10

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GCATCCGGAG

10

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

CATCCGGAGT

10

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

ATCCGGAGTA

10

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

TCCGGAGTAC

10

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

CCGGAGTACT

10

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

CGGAGTACTT

10

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GGAGTACTTC

10

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAGTACTTCA

10

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

AGTACTTCAA

10

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GTACTTCAAG

10

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

TACTTCAAGA

10

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

ACTTCAAGAA

10

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CTTCAAGAAC

10

(2) INFORMATION FOR SEQ ID NO:608:

(ii) MOLECULE TYPE: DNA

TTCAAGAACT

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

TCAAGAACTG .

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

CAAGAACTGC

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

AAGAACTGCT

10

(2) INFORMATION FOR SEO ID NO:612:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

AGAACTGCTG 10

(2) INFORMATION FOR SEQ ID NO:613:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GAACTGCTGA 10

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAAGAGATTT GGGAGAACAT GACCTGGATG CAGTGGGAAA AAGAAATTCA CAATCACACA	60
AAATACATAT ACTCCTTACT TGAAAAATCG CAGAACCAAC AAGAAAAGAA TGAACAAGAA	120
CTATTGGAAT TGGATCAATG GGCAAGTTTG TGGAATTGGT TTGACATAAC AAAATGGCTG	180
TGGTATATAA AAATATTCAT AATGGTAGTA GGAGGCTTGA TAGGTTTAAG AATAGTTTTT	240
GCTGTACTTT CTATAGTGAA TAGAGTTAGG CAGGGATACT CACCATTGTC GTTTCAGACC	300
CTCCTCCCAA CCCCAGGGG ACCCGACAGG CCCGAAGGAA TCGAAGAAGA AGGTGGAGAG	360
AGAGACAGAG ACAGATCCAC TCGATTAGTA CACGGATTCT TAGCACTTTT CTGGGACGAC	420
CTGAGGAGCC TGTGCCTCTT CCTCTACCAC CACTTGAGAG ACTTACTCTT GATTGTAACA	480
AGGATTGTGG AACTTCTGGG ACGCAGGGGA TGGGAAGCCC TCAAATATTG GTGGAACCTC	540

CTAAAGTATT GGAGCCAGGA ACTGCAGAAG AGTGCTGTTA TCTTGCTCAA TGCCACCGCC	600
ATAGCAGTAG CTGAGGGGAC AGATAGAGTT TTAGAAGTAT TACAAAGAGC TTATAGAGCT	660
ATCCTCCACA TACCTAGAAG AATAAGACAG GGCCTCGAAA TGGCTTTGCT ATAAAATGGG	720
TGGCAAGTGA GCAAAAAGTA GTGTAGTCAG ATAGCATGCA TCATAAGGGG TGGGGGCCAA	780
CAACTAACAA TGCTGATCGT GCCTGGCTAG AAGCACAAGA GAAGGAAGAA GCGGGTTTTTC	840
CAGTCAAACC TCAGGTAGCT GTAGATCTTA GCCACTTTTT AAAAGAAAAG GGGGGACTGG	900
AAGGGCTAAT TCACTCCCAA AGAAGACAAG ATACACAGTG CTGCAAACCTA TTACCAGTGG	960
AGTCAGCGAA GATAGAAGAG GCCAATGGAG GAGAAAACCA CAGATTGTTC TGTGTTGGGAC	1020
TTTCCATCCG TTGGGGACTT TCCAAGGCGG CGTGGCCTGG GTGACTAGTT CCGGTGGGGA	1080
CTTTCCAAGA AGGCGCGGCC TGGGCGGGAC TGGGGAGTGG CGAGCCCTCA GATGCTGCAT	1140
ATAAGCAGCT GCTTTCTGCT GTTACTGGGT CTCTCGGGTT AGACCAGATC TGAGCCTGGG	1200
AGCTCTCTGG CTAAGTAGGG AACCCACTGC TTAAGCCTCA ATAAAGCTTG CCTTGAGTGC	1260
TTCAAGTAGT GTGTGCCCCG CTGTTGTGTG ACTCTGGTAT CTAGA	1305

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAAACAATTT GGGATAACAT GACCTGGATG CAGTGGGAAA GAGAAATTGA CAATTACACA	60
AACATAATAT ACACCTTAAT TGAAGAATCG CAGAACCAAC AAGAAAAAAA TGAAGTAGAA	120
TTATTGGAAT TGGATAAATG GGCAAATTTG TGAATTGGT TTAGTATATC AAAGTGGCTA	180
TGGTATATAA AATTATTCAT AATGGTAGTA GGAGGCTTGG TAGGTTTAAG AATAGTTTTT	240
ACTGTACTTT CTATAGTGAA TAGAGTTAGG CAGGGATACT CACCATTGTC GTTTCAGACC	300
CACCTCCCAA CCCCAGAGG ACCCGACAGG CCAGAAGGAA TCGAAGAAGA AGGTGAGAG	360
AGAGACAGAG GCAGCTCCAC TCGATTAGTG CACGGATTCT TAGCACTTTT CTGGGACGAC	420
CTGAGGAGTC TGTGCCTCTT CAGCTACCAC CACTTGAGAG ACTTACTCTT GATTGTAACG	480
AGGATTGTGG AACTTCTGGG ACGCAGGGGA TGGGAAGCCC TCAAATACTG GTGGAATCTC	540

CTGCAGTATT GGAGGCAGGA ACTACAGAAG AGTGCTGTTA GCTTGTTCAA TGGCACGGCC	600
ATAGCAGTAG CTGAGGGGAC AGATAGAGTT ATAGAAGCTT TACGAAGGGC TTATAGAGCT	660
ATTCTCCACA TACCTAGAAG AATAAGACAG GGCTTAGAAA GGGCTTTGCT ATAAAATGGG	720
TGGCAAGTGG TCAGAAAGTA GTGTGGTTAG AAGGCATGTA CCTTTAAGAC AAGGCAGCTA	780
TAGATCTTAG CCGCTTTTTA AAAGAAAAGG GGGGACTGGA AGGGCTAATT CACTCACAGA	840
GAAGATCAGT TGAACCAGAA GAAGATAGAA GAGGCCATGA AGAAGAAAAC AACAGATTGT	900
TCCGTTTGTT CCGTTGGGGA CTTTCCAGGA GACGTGGCCT GAGTGATAAG CCGCTGGGGA	960
CTTTCCGAAG AGGCGTGACG GGAAGTTCCA AGGCGACGTG GCCTGGGCGG GACTGGGGAG	1020
TGGCGAGCCC TCAGATGCTG CATATAAGCA GCTGCTTTCT GCCTGTACTG GGTCTCTCTG	1080
GTTAGACCAG ATCTGAGCCT GGGAGCTCTC TGGCTAACTA GGGAACCCAC TGCTTAAGCC	1140
TCAATAAAGC TTGCCTTGAG TGCTTCAAGT AGTGTGTGCC CGTCTGTTGT GTGACTCTGG	1200
TATCTAGA	1208

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

TGGAAGGGCT AATTTGGT	18
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(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

ATCTTCCCTA AAAAATTAGC CTGTC	25
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(2) INFORMATION FOR SEQ ID NO:618:

(ii) MOLECULE TYPE: DNA

AGGCTCAGAT CTGGTCTAAC

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

AGCAGCAGGA AGCACTATGG

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TGCTAGAGAT TTTCCACAC

19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

AGTGAATAGA GTTAGGCAGG

20

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GTAAGACAGT ATGATCAGAT A

21

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

TTGTAGGGAA TTCCAAATTC C

21

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

CAGGATCCTA CACCTGTCAA CATAAT

26

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

00445783-050399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGGAATTCCT TATTCCTGCT TG

22

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

CCAGAAGTTC CACAATCC

18

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

TTCTTCTAGG TATGTGGAG

19

(2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

AGTGAATTAG CCCTTCCAG

19

(2) INFORMATION FOR SEQ ID NO:629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

00445-257-0000

(ii) MOLECULE TYPE: DNA

TGCTAGAGAT TTTCCACAC

19

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

TGCTCTGGAA AACTCAT

17

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

CTTTCTATAG TGAATAGAG

19

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

TATTGGAGTC AGGAACT

17

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GGTCTAACCA GAGAGAC

17

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Ala	Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala
1				5					10			

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro	Thr	Gly	Pro	Lys	Glu	Lys
1				5					10				15	
Lys	Lys	Val	Glu	Arg	Glu	Thr	Glu	Thr	Asp	Pro	Phe	Asp	Thr	Asp
			20					25					30	
Pro His														

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

Pro Ser Ser Gln Pro Arg Gly Asp Pro Thr Gly Pro Lys Glu Ser Lys
1 5 10 15
Lys Lys Val Glu Arg Glu Thr Glu Thr Asp Pro Leu Asp Tyr Thr Asp
20 25 30
Ser His

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Pro Thr Ser Gln Pro Arg Arg Asp Pro Thr Gly Gln Lys Glu Ser Lys
1 5 10 15
Lys Lys Val Glu Arg Glu Thr Glu Ala Ala Pro Leu Asp Cys Thr Asp
20 25 30
Ser His

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Asp Pro Pro Pro Asn Pro Glu Gly Thr Arg Gln Ala Arg Arg Asn Arg
1 5 10 15
Arg Arg Arg Trp Arg Glu Arg Gln Arg Gln Ile His Ser Ile Ser Glu
20 25 30
Arg Ile Leu Ser Thr Tyr Leu Gly Arg Ser Ala Glu Pro Val Pro Leu
35 40 45
Gln Leu Pro Pro Leu Glu Arg Leu Thr Leu Asp Cys Asn Glu Asp Cys
50 55 60

09146783 090398

Gly Thr Ser Gly Thr Gln Gly Val Gly Ser Pro Gln Ile Leu Val Glu
65 70 75 80
Ser Pro Thr Val Leu Glu Ser Gly Thr Lys Glu Cys Cys Leu Ala Gln
85 90 95
Cys His Ser His Ser Ser Ser Gly Asp Arg
100 105

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

Asp Pro Pro Pro Asn Pro Glu Gly Thr Arg Gln Ala Arg Arg Asn Arg
1 5 10 15
Arg Arg Arg Trp Arg Glu Arg Gln Arg Gln Ile His Ser Ile Ser Thr
20 25 30
Arg Ile Leu Ser Thr Phe Leu Gly Arg Pro Glu Glu Pro Val Pro Leu
35 40 45
Pro Leu Pro Pro Leu Glu Arg Leu Thr Leu Asp Cys Asn Lys Asp Cys
50 55 60
Gly Thr Ser Gly Thr Gln Gly Met Gly Ser Pro Gln Ile Leu Val Glu
65 70 75 80
Pro Pro Lys Val Leu Glu Pro Gly Thr Ala Glu Glu Cys Cys Tyr Leu
85 90 95
Ala Gln Cys His Arg His Ser Ser Ser Gly Asp Arg
100 105

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

Asp Pro Pro Pro Asn Pro Glu Gly Thr Arg Gln Ala Arg Arg Asn Arg
1 5 10 15

[illegible][illegible]

- [illegible]

[illegible][illegible][illegible]

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
165 170 175
Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
180 185 190
Val Asn Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
195 200 205
Arg Val Ile Glu Val Leu Gln Ala Ala Tyr Arg Ala Ile Arg His Ile
210 215 220
Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

Glu Glu Ile Trp Glu Asn Met Thr Trp Met Gln Trp Glu Lys Glu Ile
1 5 10 15
His Asn His Thr Lys Tyr Ile Tyr Ser Leu Leu Glu Lys Ser Gln Asn
20 25 30
Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Gln Trp Ala
35 40 45
Ser Leu Trp Asn Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys
50 55 60
Ile Phe Ile Met Val Val Gly Gly Leu Ile Gly Leu Arg Ile Val Phe
65 70 75 80
Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
85 90 95
Ser Phe Gln Thr Leu Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
100 105 110
Gly Ile Glu Glu Met Gly Gly Glu Arg Asp Arg Asp Arg Ser Thr Arg
115 120 125
Leu Val His Gly Phe Leu Ala Leu Phe Trp Asp Asp Leu Arg Ser Leu
130 135 140
Cys Leu Phe Leu Tyr His His Leu Arg Asp Leu Leu Leu Ile Val Thr
145 150 155 160

Arg	Ile	Val	Glu	Leu	Leu	Gly	Arg	Arg	Gly	Trp	Glu	Ala	Leu	Lys	Tyr
				165					170					175	
Trp	Trp	Asn	Leu	Leu	Lys	Tyr	Trp	Ser	Gln	Glu	Leu	Gln	Lys	Ser	Ala
			180					185					190		
Val	Ile	Leu	Leu	Asn	Ala	Thr	Ala	Ile	Ala	Val	Ala	Glu	Gly	Thr	Asp
		195					200					205			
Arg	Val	Leu	Glu	Val	Leu	Gln	Arg	Ala	Tyr	Arg	Ala	Ile	Leu	His	Ile
	210					215					220				
Pro	Arg	Arg	Ile	Arg	Gln	Gly	Leu	Glu	Met	Ala	Leu	Leu			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Glu 1	Thr	Ile	Trp	Asp 5	Asn	Met	Thr	Trp	Met 10	Gln	Trp	Glu	Arg	Glu 15	Ile
Asp	Asn	Tyr	Thr 20	Asn	Ile	Ile	Tyr	Thr 25	Leu	Ile	Glu	Glu	Ser 30	Gln	Asn
Gln	Gln	Glu 35	Lys	Asn	Glu	Leu	Glu 40	Leu	Leu	Glu	Leu	Asp 45	Lys	Trp	Ala
Asn	Leu 50	Trp	Asn	Trp	Phe	Ser 55	Ile	Ser	Asn	Trp	Leu 60	Trp	Tyr	Ile	Lys
Leu 65	Phe	Ile	Met	Val	Val 70	Gly	Gly	Leu	Val	Gly 75	Leu	Arg	Ile	Val	Phe 80
Thr	Val	Leu	Ser	Ile 85	Val	Asn	Arg	Val	Arg 90	Gln	Gly	Tyr	Ser	Pro 95	Leu
Ser	Phe	Gln	Thr 100	His	Leu	Pro	Thr	Pro 105	Lys	Gly	Pro	Asp	Arg 110	Pro	Glu
Gly	Ile	Glu 115	Glu	Glu	Gly	Gly	Glu 120	Arg	Asp	Arg	Gly	Ser 125	Ser	Thr	Arg
Leu	Val 130	His	Gly	Phe	Leu	Ala 135	Leu	Phe	Trp	Asp	Asp 140	Leu	Arg	Ser	Leu
Cys 145	Leu	Phe	Ser	Tyr	His 150	His	Leu	Arg	Asp	Leu 155	Leu	Leu	Ile	Val	Thr 160

Arg	Ile	Val	Glu	Leu	Leu	Gly	Arg	Arg	Gly	Trp	Glu	Ala	Leu	Lys	Tyr
				165					170					175	
Trp	Trp	Asn	Leu	Leu	Gln	Tyr	Trp	Arg	Gln	Glu	Leu	Gln	Lys	Ser	Ala
			180					185					190		
Val	Ser	Leu	Phe	Asn	Gly	Thr	Ala	Ile	Ala	Val	Ala	Glu	Gly	Thr	Asp
		195					200					205			
Arg	Val	Ile	Glu	Ala	Leu	Arg	Arg	Ala	Tyr	Arg	Ala	Ile	Leu	His	Ile
	210					215					220				
Pro	Arg	Arg	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Ala	Leu	Leu			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

Met 1	Gly	Gly	Lys 5	Trp	Ser	Lys	Ser	Ser	Val 10	Ile	Gly	Trp	Pro	Ala 15	Val
Arg	Glu	Arg	Met 20	Arg	Arg	Ala	Glu	Pro 25	Ala	Ala	Asp	Gly	Val 30	Gly	Ala
Val	Ser 35	Arg	Asp	Leu	Glu	Lys 40	His	Gly	Ala	Ile	Thr	Ser 45	Ser	Asn	Thr
Ala 50	Ala	Asn	Asn	Ala	Ala	Cys 55	Ala	Trp	Leu	Glu	Ala 60	Gln	Glu	Glu	Glu
Glu 65	Val	Gly	Phe	Pro	Val 70	Thr	Pro	Gln	Val	Pro 75	Leu	Arg	Pro	Met	Thr 80
Tyr	Lys	Ala	Ala	Val 85	Asp	Leu	Ser	His	Phe 90	Leu	Lys	Glu	Lys	Gly 95	Gly
Leu	Glu	Gly	Leu 100	Ile	His	Ser	Gln	Arg 105	Arg	Gln	Asp	Ile	Leu 110	Asp	Leu
Trp	Ile	Tyr 115	His	Thr	Gln	Gly	Tyr 120	Phe	Pro	Asp	Trp	Gln 125	Asn	Tyr	Thr
Pro	Gly 130	Pro	Gly	Val	Arg	Tyr 135	Pro	Leu	Thr	Phe	Gly 140	Trp	Cys	Tyr	Lys
Leu 145	Val	Pro	Val	Glu	Pro 150	Asp	Lys	Val	Glu	Glu 155	Ala	Asn	Lys	Gly	Glu 160

Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
				165						170				175	
Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His
			180					185					190		
His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys		
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

Met Gly Gly Lys Ala Lys Ser Ser Val Val Arg His Ala Ser Gly
1 5 10 15

Val Gly Ala Asn Asn Gly Cys
20

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

Met Gly Gly Lys Trp Ser Glu Ser Ser Val Val Arg Arg His Val Pro
1 5 10 15

Leu Arg Gln Gly Ser Tyr Arg Ser Pro Leu
20 25

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCTGGGCG GGA CTGGGGA 60
GTGGCGAGCC CTCA 82

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

CTGTTGGGGA CTTTCCATCC GTTGGGGACT TTCCAAGGCG GCGTGGCCTG GGTGACTAGT 60
TCCGGTGGGG ACTTTCCA 78

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

CCGTTTGTTC CGTTGGGGAC TTTCCAGGAG ACGTGGCCTG AGTGACTAAG CCGCTGGGGA 60
CTTTCCG 67

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

ATGGGTGGCA AGTGGTCAA AAGTAGTGTG ATTGGATGGC CTGCTGTAAG GGAAAGAATG 60

AGACGAGCTG AGCCAGCAGC AGATGGGGTG GGAGCAGTAT CTCGAGACCT AGAAAAACAT	120
GGAGCAATCA CAAGTAGCAA TACAGCAGCT AACAAATGCTG CTTGTGCCTG GCTAGAAGCA	180
CAAGAGGAGG AAGAGGTGGG TTTTCCAGTC ACACCTCAGG TACCTTTAAG ACCAATGACT	240
TACAAGGCAG CTGTAGATCT TAGCCACTTT TTTAAAGAAA AGGGGGGACT GGAAGGGCTA	300
ATTCACTCCC AAAGAAGACA AGATATCCTT GATCTGTGGA TCTACCACAC ACAAGGCTAC	360
TTCCCTGATT GGCAGAACTA CACACCAGGG CCAGGGGTCA GATATCCACT GACCTTTGGA	420
TGGTGCTACA AGCTAGTACC AGTTGAGCCA GATAAGGTAG AAGAGGCCAA TAAAGGAGAG	480
AACACCAGCT TGTACACCC TGTGAGCCTG CATGGAATGG ATGACCCTGA GAGAGAAGTG	540
TTAGAGTGGA GGTGTGACAG CCGCCTAGCA TTTCATCAG TGGCCCAGGA GCTGCATCCG	600
GAGTACTTCA AGAACTGCTG A	621

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GAACAGATTT GGAATAACAT GACCTGGATG GAGTGGGACA GAGAAATTAA CAATTACACA	60
AGCTTAATAC ACTCCTTAAT TGAAGAATCG CAAAACCAGC AAGAAAAGAA TGAACAAGAA	120
TTATTGGAAT TAGATAAATG GGCAAGTTTG TGAATTGGT TTAACATAAC AAATTGGCTG	180
TGGTATATAA AATTATTCAT AATGATAGTA GGAGGCTTGG TAGGTTTAAG AATAGTTTTT	240
GCTGTACTTT CTATAGTGAA TAGAGTTAGG CAGGGATATT CACCATTATC GTTTCAGACC	300
CACCTCCCAA TCCCGAGGGG ACCCGACAGG CCCGAAGGAA TAGAAGAAGA AGGTGGAGAG	360
AGAGACAGAG ACAGATCCAT TCGATTAGTG AACGGATCCT TAGCACTTAT CTGGGACGAT	420
CTGCGGAGCC TGTGCCTCTT CAGCTACCAC CGCTTGAGAG ACTTACTCTT GATTGTAACG	480
AGGATTGTGG AACTTCTGGG ACGCAGGGGG TGGGAAGCCC TCAAATATTG GTGGAATCTC	540
CTACAGTATT GGAGTCAGGA ACTAAAGAAT ACTGCTGTTA ACTTGCTCAA TGCCACAGCC	600
ATAGCAGTAG CTGAGGGGAC AGATAGGGTT ATAGAAGTAT TACAAGCAGC TTATAGAGCT	660
ATTCGCCACA TACCTAGAAG AATAAGACAG GGCTTGAAA GGATTTTGCT ATAAGATGGG	720
TGGCAAGTGG TCAAAAAGTA GTGTGATTGG ATGGCCTGCT GTAAGGGAAA GAATGAGACG	780

(2) INFORMATION FOR SEQ ID NO:652:

- (ii) MOLECULE TYPE: DNA

- GCTTTTGGCC 10

(ii) MOLECULE TYPE: DNA

- CTTTTGCCT 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

10

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

TGCCTGTACT

10

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GCCTGTACTG

10

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CCTGTACTGG

10

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

CTGTACTGGG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

10

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

CTGGGTCTCT

10

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

TGGGTCTCTC

10

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GGGTCTCTCT

10

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GGTCTCTCTG

10

00146733-000390

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

10

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

AGACCAGATC

10

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GACCAGATCT

10

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

ACCAGATCTG

10

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

CCAGATCTGA

10

004467.EC29760

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CAGATCTGAG

10

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

AGATCTGAGC

10

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GATCTGAGCC

10

(2) INFORMATION FOR SEQ ID NO:689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

ATCTGAGCCT

10

09446783-090398

10

10

10

10

(2) INFORMATION FOR SEQ ID NO:694:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

AGCCTGGGAG

10

(2) INFORMATION FOR SEQ ID NO:695:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GCCTGGGAGC

10

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

CCTGGGAGCT

10

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

CTGGGAGCTC

10

001463-09093

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TGGGAGCTCT

10

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GGGAGCTCTC

10

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GGAGCTCTCT

10

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAGCTCTCTG

10

20250923 14:54:00

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

AGCTCTCTGG

10

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GCTCTCTGGC

10

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

CTCTCTGGCT

10

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

TCTCTGGCTA

10

20250329 15:00:00

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

CTCTGGCTAA

10

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

TCTGGCTAAC

10

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

CTGGCTAACT

10

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

TGGCTAACTA

10

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GGCTAACTAG

10

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GCTAACTAGG

10

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

CTAACTAGGG

10

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

TAACTAGGGA

10

00445783-000300

(2) INFORMATION FOR SEQ ID NO:715:

- (ii) MOLECULE TYPE: DNA

AACTAGGGAA

10

(2) INFORMATION FOR SEQ ID NO:716:

- (ii) MOLECULE TYPE: DNA

ACTAGGGAAC

10

CTAGGGAACC

- (ii) MOLECULE TYPE: DNA

CTAGGGAACC

10

TAGGGAACCC

- (ii) MOLECULE TYPE: DNA

TAGGGAACCC

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

10

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

AACCCACTGC

10

(2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

ACCCACTGCT

10

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

CCCACTGCTT

10

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

CCACTGCTTA

10

001453-00033
00000-00000

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

CACTGCTTAA

10

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

ACTGCTTAAG

10

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

CTGCTTAAGC

10

(2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

TGCTTAAGCC

10

001467.00098
"EBC44160"

(2) INFORMATION FOR SEQ ID NO:730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GCTTAAGCCT

10

(2) INFORMATION FOR SEQ ID NO:731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

CTTAAGCCTC

10

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

TTAAGCCTCA

10

(2) INFORMATION FOR SEQ ID NO:733:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

TAAGCCTCAA

10

00467-0039

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

AAGCCTCAAT

10

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

AGCCTCAATA

10

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GCCTCAATAA

10

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

CCTCAATAAA

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

10

```

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

10

(2) INFORMATION FOR SEQ ID NO:742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

ATAAAGCTTG

10

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

TAAAGCTTGC

10

(2) INFORMATION FOR SEQ ID NO:744:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

AAAGCTTGCC

10

(2) INFORMATION FOR SEQ ID NO:745:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

AAGCTTGCCT

10

(2) INFORMATION FOR SEQ ID NO:746:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

AGCTTGCCTT

10

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GCTTGCCTTG

10

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

CTTGCCTTGA

10

(2) INFORMATION FOR SEQ ID NO:749:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

TTGCCTTGAG

10

(2) INFORMATION FOR SEQ ID NO:751:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GCCTTGAGTG

10

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

CTTGAGTGCT

10

10

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

TTGAGTGCTT

10

(2) INFORMATION FOR SEQ ID NO:755:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

TGAGTGCTTC

10

(2) INFORMATION FOR SEQ ID NO:756:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAGTGCTTCA

10

(2) INFORMATION FOR SEQ ID NO:757:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

AGTGCTTCAA

10

00000-00000-00000

(2) INFORMATION FOR SEQ ID NO:758:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GTGCTTCAAG

10

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

TGCTTCAAGT

10

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GCTTCAAGTA

10

(2) INFORMATION FOR SEQ ID NO:761:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

CTTCAAGTAG

10

350053-20254100

(2) INFORMATION FOR SEQ ID NO:762:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

TTCAAGTAGT

10

(2) INFORMATION FOR SEQ ID NO:763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

TCAAGTAGTG

10

(2) INFORMATION FOR SEQ ID NO:764:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

CAAGTAGTGT

10

(2) INFORMATION FOR SEQ ID NO:765:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

AAGTAGTGTG

10

00446783-00000000-00000000

(2) INFORMATION FOR SEQ ID NO:767:

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

10

(2) INFORMATION FOR SEQ ID NO:767:

- (ii) MOLECULE TYPE: DNA

GTAGTGTGTG

10

(2) INFORMATION FOR SEQ ID NO:769:

- (ii) MOLECULE TYPE: DNA

TAGTGTGTGC

10

(2) INFORMATION FOR SEQ ID NO:769:

- (ii) MOLECULE TYPE: DNA

AGTGTGTGCC

10

GTGTGTGCC 10

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GTGTGTGCC

10

TGTGTGCCCG 10

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

TGTGTGCCG

10

GTGTGCCCGT 10

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GTGTGCCCGT

10

TGTGCCCGTC 10

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

TGTGCCCGTC

10

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GTGCCCCGTCT

10

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

TGCCCCGTCTG

10

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GCCCGTCTGT

10

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

CCCGTCTGTT

10

20250909 15:54:00

(2) INFORMATION FOR SEQ ID NO:779:

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

10

(2) INFORMATION FOR SEQ ID NO:779:

- (ii) MOLECULE TYPE: DNA

CGTCTGTTGT

10

(2) INFORMATION FOR SEQ ID NO:780:

- (ii) MOLECULE TYPE: DNA

GTCTGTTGTG

10

(2) INFORMATION FOR SEQ ID NO:781:

- (ii) MOLECULE TYPE: DNA

TCTGTTGTGT

10

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

CTGTTGTGTG

10

(2) INFORMATION FOR SEQ ID NO:783:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

TGTTGTGTGA

10

(2) INFORMATION FOR SEQ ID NO:784:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GTTGTGTGAC

10

(2) INFORMATION FOR SEQ ID NO:785:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

TTGTGTGACT

10

00449460

TGTGTGACTC

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

10

GTGTGACTCT

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

10

TGTGTGACTC

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

10

GTGTGACTCT

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

10

(2) INFORMATION FOR SEQ ID NO:790:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

TGTGACTCTG

10

(2) INFORMATION FOR SEQ ID NO:791:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GTGACTCTGG

10

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

TGACTCTGGT

10

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GACTCTGGTA

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ACTCTGGTAA

- (ii) MOLECULE TYPE: DNA

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CTCTGGTAAC

- (ii) MOLECULE TYPE: DNA

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TCTGGTAACT

- (ii) MOLECULE TYPE: DNA

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CTGGTAACTA

- (ii) MOLECULE TYPE: DNA

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(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

TGGTAACTAG

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(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GGTAACTAGA

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(2) INFORMATION FOR SEQ ID NO:800:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

TGGAAGGGCT AATTCAC	TCA CGGAAAAGAC	CAGTTGAACC	AGAAGAAGAT	AGAAGAGGCC	60
ATGAAGAAGA AAACAAC	AGAGA TTGTTCTGCT	TGCTCAGCTG	GGGACTTTCC	AGAAGGCGCG	120
GCCTGAGTGA CTAAGCCCC	G TTGGGGACTT	TCCGAAGAGG	CATGAAGGGA	CTTTCCAAGG	180
CAGGCGTGGC CTGGGCGGGA	CTGGGGAGTG	GCGAGCCCTC	AGATGCTGCA	TATAAGCAGC	240
TGCTTTCTGC CTGTACTGGG	TCTCTCTGGT	TAGACCAGAT	CTGAGCCTGG	GAGCTCTCTG	300
GCTAGCTAGG GAACCCACTG	CTTAAGCCTC	AATAAAGCTT	GCCTTGAGTG	CTTCAAGTAG	360
TGTGTGCCCCG TCTGTTGTGT	GACTCTGGTA	TCTAGAGATC	CCTCAGACCA	TTTTAGTCCG	420
TGTGGAAAAT CTCTAGCAGT	GGCGCCCGAA	CAGGGACTTG	AAAGCGAAAG	GAAAACCAGA	480

GGAGCTCTCT	CGACGCAGGA	CTCGGCTTGC	TGAAGCGCGC	ACGGCAAGAG	GCGAGGGGCG	540
GCGACTGGTG	AGTACGCCGA	AAATTTTGAC	TAGCGGAGGC	TAGAAGGAGA	GAGATGGGTG	600
CGAGAGCGTC	AATATTAAGC	GGGGGAAAAT	TAGATAGATG	GGAGAAAATT	CGGTTAAGGC	660
CAGGAGGAAA	GAAAAAGTAT	AAATTTAAAC	ATATAGTATG	GGCAAGCAGG	GAGCTAGAAC	720
GATTTCGAGT	CAATCCTGGC	CTGTTGGAAA	CATCAGAAAG	CTGTAGACAA	ATACTGGGAC	780
AGTTACACCC	GTCCCTTCAG	ACAGGATCAG	AAGAACTTAA	ATCAGTATAT	AATGCAGTAG	840
CAGTCTCTTA	TTGTGTGCAT	CAAAACATAG	ACATAAAGGA	CACCAAGGAA	GCTTTAGAAA	900
AGATAGAGGA	AGAGCAAAAC	AAATGTAAGA	AAAAAGCACA	GCAAGCAGCA	GCACAGCAAG	960
CAGCAGCTGG	CACAGGAAAC	AGCAACCCGG	TCAGCCAAAA	TTACCCTATA	GTACAGAACA	1020
TGCAGGGGCA	AATGGTACAT	CAGGCCATAT	CACCTAGAAC	TTTAAATGCA	TGGGTAAAAG	1080
TAATAGAAGA	GAAGGCTTTC	AGCCCAGAGG	TAATACCCAT	GTTTTCAGCA	TTATCAGAAG	1140
GAGCCACCCC	ACAAGATTTA	AACACCATGC	TAAACACAGT	GGGGGGACAT	CAAGCAGCTA	1200
TGCAATGTT	AAAAGAGACC	ATCAATGAGG	AAGCTGCAGA	ATGGGATAGA	TTACATCCAG	1260
CGCAGGCAGG	GCCTGTTGCA	CCAGGCCAGA	TGAGAGACCC	AAGGGGAAGT	GACATAGCAG	1320
GAACTACTAG	TACCCTTCAG	GAACAAATAG	GATGGATGAC	AGGTAATCCA	GCTATCCCAG	1380
TAGGAGAAAT	CTATAAAAGA	TGGATAATCC	TGGGATTAAA	TAAATAGTA	AGGATGTATA	1440
GCCCTATCAG	CATTCTGGAC	ATAAAACAAG	GACCAAAGGA	ACCTTTTAGA	GA CTATGTAG	1500
ACCGGTTCTA	TAAAACTCTA	AGAGCCGAGC	AAGCTACACA	GGAGGTAAAA	AATTGGATGA	1560
CAGAAACCTT	GTGGGTCCAA	AATGCAAACC	CAGATTGTAA	GA CTATTTTA	AAAGCATTGG	1620
GACCAGCAGC	TACACTAGAA	GAAATGATGA	CAGCATGTCA	GGGAGTGGGA	GGACCCAGCC	1680
ATAAAGCAAG	AGTTTTGGCA	GAAGCAATGA	GCCAAGCAAC	AAATGCAGCT	ACTGTAATGA	1740
TGCAGAGAAG	CAATTTTAGA	AACCAAAGAA	AGAATGTTAA	GTGTTTCAAT	TGTGGCAAAG	1800
AAGGGCACAT	AGCCAGAAAT	TGCAGGGCTC	CTAGGAAAAG	GGGCTGTTGG	AAATGTGGAA	1860
AGGAAGGACA	CCAAATGAAA	GATTGTACTG	AGAGACAGGC	TAATTTTTTA	GGGAAATCT	1920
GGCCTTCCCA	CAAGGGGAGG	CCAGGGA ACT	TTCTTCAGAG	CAGGCCAGAA	CCAACAGCCC	1980
CTCTCCAGGG	CAGGCCGAG	CCATCAGCCC	CGCCAGAAGA	GAGCTTCAGG	TTTGGGGAGG	2040
AGACAACAAC	TCCCTCTCAG	AAGCAGGAGC	CGATAGACAG	GGACAGGGAT	CTGTATCCTT	2100
TAGCTTCCCT	CAGATCACTC	TTTGGCAACG	ACCCCTCGTC	ACAATAAAGA	TAGGGGGGCA	2160
GCTGAAGGAA	GCTCTATTAG	ATACAGGAGC	AGATGATACA	GTATTAGAAG	ACATGCATTT	2220
GCCAGGAAAA	TGGAAACCAA	AAATGATAGG	GGGAATTGGA	GGTTTTATCA	AAGTAAAACA	2280

ATATGATGAA	ATTCTTGTAG	AAATCTGTGG	ACATAAAGCT	ATAGGTACAG	TATTAGTAGG	2340
ACCTACACCT	GTCAACATAA	TTGGAAGAAA	TCTGTTGACT	CAGATTGGTT	GCACTTTAAA	2400
TTTTCCCATT	AGTCCTATTG	AAACTGTACC	AGTACAATTA	AAGCCAGGAA	TGGATGGCCC	2460
AAAGGTTAAA	CAATGGCCAT	TGACAGAAGA	GAAAATAAAA	GCATTAGTAG	AAATTTGTAC	2520
AGAAATGGAA	AAGGAAGGAA	AGATTTCAAA	AATTGGGCCT	GAAAATCCAT	ACAATACTCC	2580
AGTATTTGCC	ATAAAGAAAA	AAGATGGTAC	TAAATGGAGA	AAATTAGTAG	ATTTTCAGAGA	2640
CCTTAATAAG	AGAACTCAAG	ACTTCTGGGA	AGTTCAATTA	GGAATACCAC	ATCCCTCAGG	2700
ATTAAAAAAG	AAAAAATCAG	TAACAGTACT	GGATGTGGGT	GATGCATACT	TTTCAGTTCC	2760
CTTAGATGAA	AACTTCAGGA	AGTATACTGC	ATTTACCATA	CCTAGTATAA	ATAATGAGAC	2820
ACCAGGGATT	AGATATCAGT	ACAATGTGCT	TCCACAGGGA	TGGAAAGGAT	CACCAGCAAT	2880
ATTCCAAAGT	AGCATGACAA	GAATCTTAGA	GCC'TTTTAGA	AGACAAAATC	CAGACATAGT	2940
TATCTATCAA	TACATGGATG	ACTTGTATGT	AGGATCTGAT	TTAGAAATAG	GACAGCATAG	3000
AATAAAAATA	GAGGAACTGA	GACAACATCT	GTTGAAAGTG	GGATTTACCA	CACCAGACAA	3060
AAAGCATCAG	AAAGAACCCC	CATTCCTTTG	GATGGGTTAT	GAACTCCATC	CTGATAAATG	3120
GACAGTGCAA	CCTATAGTAC	TGCCAGAAAA	AGACAGCTGG	ACTGTCAATG	ACATACAGAA	3180
GTTAGTGGGT	AAATTAAATT	GGGCAAGTCA	GATTTACCCA	GGAATTAAAG	TAAGGCAATT	3240
ATGTAAACTC	CTTAGGGGAA	CCAAAGCACT	AACAGAAGTA	ATACCACTAA	CAGAAGAAGC	3300
AGAGCTAGAA	CTGGCAGAAA	ACAGGGAAAT	TCTAAGAGAA	CCAGTACATG	GAGTGTATTA	3360
TGACCCATCA	AAAGACTTAA	TAGCAGAAAT	ACAGAAGCAG	GAGCAAGGCC	AATGGACATA	3420
TCAAATTTAT	CAAGATCAAT	TTAAAAATCT	AAAAACAGGA	AAGTATGCAA	GATTGAGGGG	3480
TGCCCACACT	AATGATGTAA	AACAATTTCC	AGAGGCAGTG	CAAAAAATAG	CCACAGAAAG	3540
CATAGTAATA	TGGGGAAAGA	CTCCTAAATT	TAGACTACCC	ATACAAAAAG	AAACATGGGA	3600
CGCATGGTGG	ACAGAGTATT	GGCAAGCCAC	CTGGATTCCCT	GAGTGGGAGT	TTGTCAATAC	3660
CCCTCCCCTA	GTAAATTAT	GGTACCAGTT	AGAAAAAGAA	CCCATAATAG	GAGCAGAAAC	3720
TTTCTATGTA	GATGGGGCAG	CTAACAGAGA	GACTAAATTA	GGAAAAGCAG	GATATGTTAC	3780
TGACAGAGGA	AGACAAAAAG	TTGTCTCCCT	AACTGACACA	ACAAATCAGA	AGACTGAGTT	3840
ACAAGCAATT	CATCTAGCTT	TGCAGGATTC	AGGATTAGAA	GTAAACATAG	TAACAGACTC	3900
ACAGTATGCA	TTAGGAATCA	TTCAAGCACA	ACCAGATAAA	AGTGAATCAG	AAATAGTCAA	3960
TCAAATAATA	GAGCAATTAA	TAAAAAAGGA	AAAGGTCTAC	CTGGCATGGG	TACCAGCACA	4020
CAAAGGAATT	GGAGGGGAATG	AACAAGTAGA	TAAATTAGTC	AGTGCTGGAA	TCAGGAAAAT	4080

ACTATTTT	TATGGAATAG	ATAAGGCACA	AGAAGGCCAT	GAGAAATATC	ACAGTAATTG	4140
GAGAGCAATG	GCTAGTGGTT	TTAACCTGCC	ACCTATAGTA	GCAAAAGAAA	TAGTAGCCAG	4200
CTGTGATAAA	TGTCAGCTAA	AAGGAGAAGC	CATGCATGGA	CAAGTAGACT	GTAGTCCAGG	4260
AATATGGCAA	CTAGATTGTA	CACATCTAGA	AGGAAAAATT	ATCCTGGTAG	CAGTTCATGT	4320
AGCCAGTGGA	TATATAGAAG	CAGAAGTTAT	TCCAGCAGAG	ACAGGGCAGG	AAACAGCATA	4380
CTTTATCTTA	AAATTAGCAG	GAAGGTGGCC	AGTAAACACA	ATACATACAG	ACAAATGGCGG	4440
CAATTTTCATC	AGTACCACGG	TTAAGGCCGC	CTGTTGGTGG	GCAGGGATCA	AGCAGGAATT	4500
TGGCATTCCC	TACAATCCCC	AAAGCCAAGG	AGTAGTGGA	TCTATGAATA	GAGAATTAAA	4560
GAAAATTATA	GGACAGGTAA	GAGATCAGGC	TGAACATCTT	AAGACAGCAG	TACAAATGGC	4620
AGTATTCATC	CACAATTTTA	AAAGAAAAGG	GGGGATTGGG	GGATACAGTG	CAGGGGAAAG	4680
AATAGTAGAC	ATAATAGCAA	CAGACATACA	AACTAAAGAA	TTACAAAAGC	AAATTACAAA	4740
AATTCAAAAT	TTTCGGGTTT	ATTACAGGGA	CAGCAGAGAT	CCACTTTGGA	AAGGACCAGC	4800
AAAACCTTCTC	TGGAAGGCG	AAGGGGCAGT	AGTAATACAA	GATAATAGTG	ACATAAAAGT	4860
AGTGCCAAGA	AGAAAAGTAA	AGATCATTAG	GGATTATGGA	AAACAGATGG	CAGGTGATGA	4920
TTGTGTGGCA	AGTAGACAGG	ATGAGGATTA	GAACATGGAA	CAGTTTAGTG	AAACACCATA	4980
TGTATGTTTC	AAAGAAAGCT	AAGGGATGGA	TTTATAGACA	TCACTATGAA	AACACTCATC	5040
CAAAAATAAG	CTCAGAAGTA	CACATCCCAC	TAGGGGAAGC	TAGATTGGTA	ATAACAACAT	5100
ATTGGGGTCT	ACATACAGGA	GAAAGAGACT	GGCATTTGGG	TCAGGGAGTC	TCCATAGAAT	5160
GGAGGGAAAG	GACATATAGA	ACACAAGTAG	ACCCCGAACT	AGCAGACCAA	CTAATTCTATA	5220
TACATTACTT	TGATTGTTTT	TCAGAACTCG	CCATAAGAAG	TGCCATATTA	GGATATAGAG	5280
TTAGGCATAG	GTGTGAATAT	CAAGCAGGAC	ATAACAAGGT	AGGATCTCTA	CAGTACTTGG	5340
CACTAACAGC	ATTAATAACA	CCAAAGAAGA	TAAAGCCACC	TTTGCCTAGT	GTTGCGAAAC	5400
TGACAGAGGA	TAGATGGAAC	AAGCCCCAGA	AGACCAAGGG	CCACAGAGGC	AGCCATACAA	5460
TGAATGGACA	CTAGAACTTT	TAGAGGAGCT	TAAGAATGAA	GCTGTTAGGC	ATTTTCCTAG	5520
GGTATGGCTC	CATGGCTTAG	GGCAACATAT	CTATGAAACT	TATGGGGATA	CTTGGGAAGG	5580
AGTGAGAGCC	ATAACAAGAA	CTCTGCAACA	ACTGCTGTTT	ATTCAATTTCA	GAATTGGGTG	5640
TCAACATAGC	AGAATAGGCA	TTATTTCGACA	GAGGAGAGCA	AGAAATGGAG	CCAGTAGATC	5700
CTAGACTAGA	GCCCTGGAAG	CATCCAGGAA	GTCAGCCTAA	GACTGCGTGT	ACCACTTGCT	5760
ATTGTAAAAA	GTGCTGCTTT	CATTGCCAAG	TTTGTTTTAT	GACAAAAGGC	TTAGGCATCT	5820
CCTATGGCAG	GAAGAAGCGG	AGACAGCGAC	GAAGAGCTCC	TCAAGACAGT	CAGACTCATC	5880

AAGCTTATCT	ATCAAAGCAG	TAAGTAATAT	ATGTAATGCA	ACCTTTACAA	ATAGTAGCAA	5940
TAGTAGCATT	AGTAGTAGCA	GGAATAATAG	CAATAGTTGT	GTGGACCATA	GTATTCATAG	6000
AATATAAGAA	AATATTAAGA	CAAAGAAAAA	TAGACAGGTT	GATTGATAGA	ATAAGAGAAA	6060
GAGCAGAAGA	CAGTGGCAAT	GACAGTGAAG	GGGATCAGGA	AGAATTATCG	GCACTTGTGG	6120
ACATGGGGCA	CCATGATCCT	TGGGATATTA	ATGATCTGTA	GAGCTGCAAA	CAATTTGTGG	6180
GTCACAGTCT	ATTATGGGGT	ACCTGTGTGG	AGAGAAGCAA	CCACCACTCT	ATTTTGTGCA	6240
TCAGATGCCA	AGGCATATGA	TGCAGAGGTA	CATAATGTTT	GGGCCACACA	TGCCTGTGTA	6300
CCCACAGACC	CTAACCCACA	AGAAGTAGAA	TTGAAAAATG	TGACAGAAAA	TTTTAACATG	6360
TGGAAAAATA	ACATGGTAGA	ACAGATGCAT	GAGGATATAA	TCAGTTTATG	GGATCAAAGC	6420
CTGAAGCCAT	GTGTAAAATT	AACCCCACTC	TGTGTTTCTT	TAAATTGCAC	TGATGCTACT	6480
AATACCACTA	ATAGTAATAC	CACTAGCAGC	AGCGAGAAAC	CGAAGGGGAC	AGGGGAAATA	6540
AAAAACTGCT	CTTTCAATAT	CACCACAAGC	ATAAGAGATA	AGGTGCAGAA	ACAATATGCA	6600
CTTTTTTATA	GCCTTGATGT	AGTACCAATG	GATGATAATG	ATAATAGTAC	AAGCTATAGG	6660
TTAATAAGTT	GTAACACCTC	AATCATTACA	CAGGCCTGTC	CAAAGATATC	CTTTGAGCCA	6720
ATTCCCATAC	ATTATTGTGC	CCCGGCTGGT	TTTGCGATTC	TAAAGTGTA	AGATAAAAGG	6780
TTCAATGGAA	AAGGACCATG	TACAAGTGTC	AGCACAGTAC	AGTGACACA	TGGAATTAGG	6840
CCAGTAGTAT	CAACTCAACT	GTTGTAAAT	GGCAGTCTAG	CAGAAGAAGA	GGTAGTAATT	6900
AGATCTGACA	ATTTTACGAA	CAATGCTAAA	ACCATAATAG	TACAGCTGAG	CAAATCTGTA	6960
GAAATTACTT	GTGTAAGACC	CAACAACAAT	ACAAGAAAAA	GTATAAGTAT	GGGACCAGGG	7020
AGAGCATTTT	ATACAACAGA	AATAATAGGA	GATATAAGAC	AAGCATATTG	TAACATTAGT	7080
AAAGCAAAC	GGACTGACAC	TTTAGAACAG	ATAGCTAGAA	AATTAAGAGA	ACAATTTGAG	7140
AATAAAACAA	TAGTCTTTAA	GCCATCCTCA	GGAGGGGACC	CAGAAATTGT	AACACAGTTT	7200
TACAGTTTTA	ATTGTGGAGG	GGAATTTTTC	TACTGTAATT	CAACACAAC	GTTTAATGGT	7260
ACTTGGAATG	GTAATTGGGT	TAATGGTACT	TGGAGTAGTA	ATAATACGAC	TGATACTGCA	7320
AATATCACAC	TCCCATGCAG	AATAAAACAA	TTTATAAACA	TGTGGCAGGA	AGTAGGAAAA	7380
GCAATGTATG	CCCCTCCCAT	CAAAGGACAA	ATTAAATGTA	CATCAAATAT	TACAGGGCTG	7440
ATATTAACAA	GAGATGGTGG	TAACAATAAC	ACCACGAACG	ACAACGAGAC	CGAGACCTTC	7500
AGACCTGGAG	GAGGAGATAT	GAGGGACAAT	TGGAGAAGTG	AATTATATAA	ATATAAAGTA	7560
GTACAAGTTG	AACCATTAGG	AGTAGCACCC	ACCAAGGCAA	AGAGAAGAGT	GGTGCAAAGA	7620
GAAAAAAGAG	CAGTGGGAAT	AGGAGCTATG	TTCCTTGGGT	TCTTAGGAGC	AGCAGGAAGC	7680

ACTATGGGCG CAGCGTCAGT GACGCTGACG GTACAAGCCA GACAATTATT GTCTGGTATA	7740
GTGCAGCAGC AGAACAATCT GCTGAGGGCT ATTGAGGCGC AACAGCATCT GTTGCAACTC	7800
ACAGTCTGGG GCATCAAACA GCTCCAGGCA AGAGTCCTGG CTGTGGAAAG ATACCTAAGG	7860
GATCAACAGC TCCTGGGACT TTGGGGTTGC TCTGGAAAAC TCATTTGCAC CACTACTGTG	7920
CCTTGGAACA ATAGCTGGAG TAATAAATCT CTGGAAACAA TTTGGGATAA CATGACCTGG	7980
ATGCAGTGGG AAAGAGAAAT TGACAATTAC ACAAACATAA TATACACCTT AATTGAAGAA	8040
TCGCAGAACC AACAAGAAAA AAATGAACTA GAATTATTGG AATTGGATAA ATGGGCAAAT	8100
TTGTGGAATT GGTTTAGTAT ATCAAACCTG CTATGGTATA TAAAATTATT CATAATGGTA	8160
GTAGGAGGCT TGGTAGGTTT AAGAATAGTT TTTACTGTAC TTTCTATAGT TAATAGAGTT	8220
AGGCAGGGAT ACTCACCATT ATCGTTTCAG ACCCACCTCC CAACCCCGAA GGGACCCGAC	8280
AGGCCAGAAG GAATCGAAGA AGAAGGTGGA GAGAGAGACA GAGGCAGCTC CACTCGATTA	8340
GTGCACGGAT TCTTAGCACT TTTCTGGGAC GACCTGAGGA GTCTGTGCCT CTTCAGCTAC	8400
CACCACTTGA GAGACTTACT CTTGATTGTA ACGAGGATTG TGGAACCTCT GGGACGCAGG	8460
GGATGGGAAG CCCTCAAATA CTGGTGGAAT CTCCTGCAGT ATTGGAGGCA GGAACCTACAG	8520
AAGAGTGCTG TTAGCTTGTT CAATGGCACG GCCATAGCAG TAGCTGAGGG GACAGATAGA	8580
GTTATAGAAG CTTTACGAAG GGCTTATAGA GCTATTCTCC ACATACCTAG AAGAATAAGA	8640
CAGGGCTTAG AAAGGGCTTT GCTATAAAAT GGGTGGCAAG TGGTCAGAAA GTAGTGTGGT	8700
TAGAAGGCAT GTACCTTTAA GACAAGGCAG CTATAGATCT TAGCCGCTTT TAAAAGAAA	8760
AGGGGGGACT GGAAGGGCTA ATTCACTCAC GGAAAAGACC AGTTGAACCA GAAGAAGATA	8820
GAAGAGGCCA TGAAGAAGAA AACAACAGAT TGTTCCTGCTT GCTCAGCTGG GGACTTTCCA	8880
GAAGGCGCGG CCTGAGTGAC TAAGCCCCGT TGGGGACTTT CCGAAGAGGC ATGAAGGGAC	8940
TTTCCAAGGC AGGCGTGGCC TGGGCGGGAC TGGGGAGTGG CGAGCCCTCA GATGCTGCAT	9000
ATAAGCAGCT GCTTCTGCC TGTACTGGGT CTCTCTGGTT AGACCAGATC TGAGCCTGGG	9060
AGCTCTCTGG CTAGCTAGGG AACCCACTGC TTAAGCCTCA ATAAAGCTTG CCTTGAGTGC	9120
TTCAAGTAGT GTGTGCCCCG CTGTTGTGTG ACTCTGGTAT CTAGAGATCC CTCAGACCAT	9180
TTTAGTCCGT GTGGAAAATC TCTAGCA	9207

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

ACCAGCTTGT TACACCCTGT GAGCCTGCAT GGAATGGATG ACCCTGAG

48

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

ACCAGCTTGT

10

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

CCAGCTTGTT

10

(2) INFORMATION FOR SEQ ID NO:805:

0445737-09099

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

CAGCTTGTTA

10

(2) INFORMATION FOR SEQ ID NO:806:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

AGCTTGTTAC

10

(2) INFORMATION FOR SEQ ID NO:807:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

GCTTGTTACA

10

(2) INFORMATION FOR SEQ ID NO:808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

CTTGTTACAC

10

(2) INFORMATION FOR SEQ ID NO:809:

09145783-090398
366060-2824160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

TTGTTACACC

10

(2) INFORMATION FOR SEQ ID NO:810:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

TGTTACACCC

10

(2) INFORMATION FOR SEQ ID NO:811:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

GTTACACCCT

10

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

TTACACCCTG

10

(2) INFORMATION FOR SEQ ID NO:813:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

TACACCCTGT

10

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ACACCCTGTG

10

(2) INFORMATION FOR SEQ ID NO:815:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

CACCCTGTGA

10

(2) INFORMATION FOR SEQ ID NO:816:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

ACCCTGTGAG

10

(2) INFORMATION FOR SEQ ID NO:817:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

CCCTGTGAGC

10

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

CCTGTGAGCC

10

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

CTGTGAGCCT .

10

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

TGTGAGCCTG

10

(2) INFORMATION FOR SEQ ID NO:821:

00145783-000350

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GTGAGCCTGC

10

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

TGAGCCTGCA

10

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GAGCCTGCAT

10

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

AGCCTGCATG

10

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GCCTGCATGG

10

(2) INFORMATION FOR SEQ ID NO:826:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

CCTGCATGGA .

10

(2) INFORMATION FOR SEQ ID NO:827:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

CTGCATGGAA

10

(2) INFORMATION FOR SEQ ID NO:828:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

TGCATGGAAT

10

(2) INFORMATION FOR SEQ ID NO:829:

09446703-090399

(ii) MOLECULE TYPE: DNA

GCATGGAATG

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

CATGGAATGG

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

ATGGAATGGA

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

TGG AATGGAT

10

(2) INFORMATION FOR SEQ ID NO:833:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GGAATGGATG

10

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATGGATGA

10

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

AATGGATGAC

10

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ATGGATGACC

10

(2) INFORMATION FOR SEQ ID NO:837:

00446300-EBZ94160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

TGGATGACCC

10

(2) INFORMATION FOR SEQ ID NO:838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GGATGACCCT

10

(2) INFORMATION FOR SEQ ID NO:839:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GATGACCCTG

10

(2) INFORMATION FOR SEQ ID NO:840:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

ATGACCCTGA

10

(2) INFORMATION FOR SEQ ID NO:841:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

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- 212 -

CLAIMS:

1. An isolated HIV-1 strain or a component, part, fragment or derivative thereof which is substantially non-pathogenic.
2. A strain of HIV-1 according to claim 1 wherein said strain is capable of stimulating an immune response in a human or primate against at least one glycoprotein on HIV-1 whilst not substantially reducing proliferative responses and cytokine production to a mitogen in said human or primate compared to a healthy, non-infected human or primate subject.
3. A strain of HIV-1 according to claim 2 which carries one or more mutations in its genome resulting in the inability to direct synthesis of at least one polypeptide or protein from a pathogenic strain of HIV-1 or results in reduced synthesis of said polypeptide or protein.
4. A strain of HIV-1 according to claim 2 which carries one or more mutations in its genome resulting in the said genome directing synthesis of a truncated form of a polypeptide or protein from a pathogenic strain of HIV-1.
5. A strain of HIV-1 according to claim 3 or 4 wherein said strain carries a mutation in its *nef* gene and/or long terminal repeat (LTR) region or in a functionally equivalent location in the HIV-1 genome.
6. A strain of HIV-1 according to claim 5 wherein said strain is reactive to antibodies to gp41-45, gp120 and/or gp160 of HIV-1 and carries a deletion of at least ten contiguous nucleotides in a region corresponding to the *nef* gene and/or LTR region of pathogenic HIV-1.
7. A strain of HIV-1 according to claim 6 wherein said strain encodes a modified Nef protein without amino acids 162 to 177 of wild-type HIV-1_{NL43} Nef.

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- 213 -

8. A strain of HIV-1 according to claim 6 or 7 wherein said strain is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env*.

9. A strain of HIV-1 according to claim 8 wherein said strain carries a deletion in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43}.

10. A strain of HIV-1 according to claim 9 wherein said strain carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(i)	8830-8862;
	(ii)	9009-9035;
	(iii)	9019-9029; and
	(iv)	9033-9049.

11. A strain of HIV-1 according to claim 9 wherein said strain carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(v)	9281-9371;
	(vi)	9281-9362;
	(vii)	9105-9224; and
	(viii)	9271-9370.

12. A strain of HIV-1 according to claim 9 wherein said strain carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(ix)	8882-8928;
	(x)	8850-9006;
	(xi)	8792-9041; and
	(xii)	9112-9204.

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950606, p10per/agh, HTV1, USA, ...

950606.pctoper/hjb,HIV1.U3-14

- 214 -

13. A strain of HIV-1 according to claim 9 wherein said strain carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(xiii)	9105-9224
	(xiv)	9389-9395; and
	(xv)	9281-9366.

14. A strain of HIV-1 according to claim 9 wherein said deletion encompasses at least one of the following decanucleotides from the *nef* gene of HIV-1_{NL43}:

ATGGGTGGCA (SEQ ID NO:2);	TGGGTGGCAA (SEQ ID NO:3);
GGGTGGCAAG (SEQ ID NO:4);	GGTGGCAAGT (SEQ ID NO:5);
GTGGCAAGTG (SEQ ID NO:6);	TGGCAAGTGG (SEQ ID NO:7);
GGCAAGTGGT (SEQ ID NO:8);	GCAAGTGGTC (SEQ ID NO:9);
CAAGTGGTCA (SEQ ID NO:10);	AAGTGGTCAA (SEQ ID NO:11);
AGTGGTCAAA (SEQ ID NO:12);	GTGGTCAAAA (SEQ ID NO:13);
TGGTCAAAAA (SEQ ID NO:14);	GGTCAAAAAG (SEQ ID NO:15);
GTCAAAAAGT (SEQ ID NO:16);	TCAAAAAGTA (SEQ ID NO:17);
CAAAAAGTAG (SEQ ID NO:18);	AAAAAGTAGT (SEQ ID NO:19);
AAAAGTAGTG (SEQ ID NO:20);	AAAGTAGTGT (SEQ ID NO:21);
AAGTAGTGTG (SEQ ID NO:22);	AGTAGTGTGA (SEQ ID NO:23);
GTAGTGTGAT (SEQ ID NO:24);	TAGTGTGATT (SEQ ID NO:25);
AGTGTGATTG (SEQ ID NO:26);	GTGTGATTGG (SEQ ID NO:27);
TGTGATTGGA (SEQ ID NO:28);	GTGATTGGAT (SEQ ID NO:29);
TGATTGGATG (SEQ ID NO:30);	GATTGGATGG (SEQ ID NO:31);
ATTGGATGGC (SEQ ID NO:32);	TTGGATGGCC (SEQ ID NO:33);
TGGATGGCCT (SEQ ID NO:34);	GGATGGCCTG (SEQ ID NO:35);
GATGGCCTGC (SEQ ID NO:36);	ATGGCCTGCT (SEQ ID NO:37);
TGGCCTGCTG (SEQ ID NO:38);	GGCCTGCTGT (SEQ ID NO:39);
GCCTGCTGTA (SEQ ID NO:40);	CCTGCTGTAA (SEQ ID NO:41);
CTGCTGTAAG (SEQ ID NO:42);	TGCTGTAAGG (SEQ ID NO:43);
GCTGTAAGGG (SEQ ID NO:44);	CTGTAAGGGA (SEQ ID NO:45);
TGTAAGGGAA (SEQ ID NO:46);	GTAAGGGAAA (SEQ ID NO:47);
TAAGGGAAAG (SEQ ID NO:48);	AAGGGAAAGA (SEQ ID NO:49);
AGGGAAAGAA (SEQ ID NO:50);	GGGAAAGAAT (SEQ ID NO:51);
GGAAAGAATG (SEQ ID NO:52);	GAAAGAATGA (SEQ ID NO:53);

00446783-000399

950606.p\oper\ajh_HIV1.US. 15

- 215 -

AAAGAATGAG (SEQ ID NO:54);	AAGAATGAGA (SEQ ID NO:55);
AGAATGAGAC (SEQ ID NO:56);	GAATGAGACG (SEQ ID NO:57);
AATGAGACGA (SEQ ID NO:58);	ATGAGACGAG (SEQ ID NO:59);
TGAGACGAGC (SEQ ID NO:60);	GAGACGAGCT (SEQ ID NO:61);
AGACGAGCTG (SEQ ID NO:62);	GACGAGCTGA (SEQ ID NO:63);
ACGAGCTGAG (SEQ ID NO:64);	CGAGCTGAGC (SEQ ID NO:65);
GAGCTGAGCC (SEQ ID NO:66);	AGCTGAGCCA (SEQ ID NO:67);
GCTGAGCCAG (SEQ ID NO:68);	CTGAGCCAGC (SEQ ID NO:69);
TGAGCCAGCA (SEQ ID NO:70);	GAGCCAGCAG (SEQ ID NO:71);
AGCCAGCAGC (SEQ ID NO:72);	GCCAGCAGCA (SEQ ID NO:73);
CCAGCAGCAG (SEQ ID NO:74);	CAGCAGCAGA (SEQ ID NO:75);
AGCAGCAGAT (SEQ ID NO:76);	GCAGCAGATG (SEQ ID NO:77);
CAGCAGATGG (SEQ ID NO:78);	AGCAGATGGG (SEQ ID NO:79);
GCAGATGGGG (SEQ ID NO:80);	CAGATGGGGT (SEQ ID NO:81);
AGATGGGGTG (SEQ ID NO:82);	GATGGGGTGG (SEQ ID NO:83);
ATGGGGTGGG (SEQ ID NO:84);	TGGGGTGGGA (SEQ ID NO:85);
GGGGTGGGAG (SEQ ID NO:86);	OGGTGGGAGC (SEQ ID NO:87);
GGTGGGAGCA (SEQ ID NO:88);	GTGGGAGCAG (SEQ ID NO:89);
TGGGAGCAGT (SEQ ID NO:90);	GGGAGCAGTA (SEQ ID NO:91);
GGAGCAGTAT (SEQ ID NO:92);	GAGCAGTATC (SEQ ID NO:93);
AGCAGTATCT (SEQ ID NO:94);	GCAGTATCTC (SEQ ID NO:95);
CAGTATCTCG (SEQ ID NO:96);	AGTATCTCGA (SEQ ID NO:97);
GTATCTCGAG (SEQ ID NO:98);	TATCTCGAGA (SEQ ID NO:99);
ATCTCGAGAC (SEQ ID NO:100);	TCTCGAGACC (SEQ ID NO:101);
CTCGAGACCT (SEQ ID NO:102);	TCGAGACCTA (SEQ ID NO:103);
CGAGACCTAG (SEQ ID NO:104);	GAGACCTAGA (SEQ ID NO:105);
AGACCTAGAA (SEQ ID NO:106);	GACCTAGAAA (SEQ ID NO:107);
ACCTAGAAAA (SEQ ID NO:108);	CCTAGAAAAA (SEQ ID NO:109);
CTAGAAAAAC (SEQ ID NO:110);	TAGAAAAACA (SEQ ID NO:111);
AGAAAAACAT (SEQ ID NO:112);	GAAAAACATG (SEQ ID NO:113);
AAAAACATGG (SEQ ID NO:114);	AAACATGGA (SEQ ID NO:115);
AAACATGGAG (SEQ ID NO:116);	AACATGGAGC (SEQ ID NO:117);
ACATGGAGCA (SEQ ID NO:118);	CATGGAGCAA (SEQ ID NO:119);
ATGGAGCAAT (SEQ ID NO:120);	TGGAGCAATC (SEQ ID NO:121);
GGAGCAATCA (SEQ ID NO:122);	GAGCAATCAC (SEQ ID NO:123);
AGCAATCACA (SEQ ID NO:124);	GCAATCACAA (SEQ ID NO:125);
CAATCACAAG (SEQ ID NO:126);	AATCACAAGT (SEQ ID NO:127);
ATCACAAGTA (SEQ ID NO:128);	TCACAAGTAG (SEQ ID NO:129);

001457-00030

950606.pctoper@hiv1.US-216

- 216 -

CACAAGTAGC (SEQ ID NO:130);	ACAAGTAGCA (SEQ ID NO:131);
CAAGTAGCAA (SEQ ID NO:132);	AAGTAGCAAT (SEQ ID NO:133);
AGTAGCAATA (SEQ ID NO:134);	GTAGCAATAC (SEQ ID NO:135);
TAGCAATACA (SEQ ID NO:136);	AGCAATACAG (SEQ ID NO:137);
GCAATACAGC (SEQ ID NO:138);	CAATACAGCA (SEQ ID NO:139);
AATACAGCAG (SEQ ID NO:140);	ATACAGCAGC (SEQ ID NO:141);
TACAGCAGCT (SEQ ID NO:142);	ACAGCAGCTA (SEQ ID NO:143);
CAGCAGCTAA (SEQ ID NO:144);	AGCAGCTAAC (SEQ ID NO:145);
GCAGCTAACA (SEQ ID NO:146);	CAGCTAACAA (SEQ ID NO:147);
AGCTAACAAT (SEQ ID NO:148);	GCTAACAATG (SEQ ID NO:149);
CTAACAATGC (SEQ ID NO:150);	TAACAATGCT (SEQ ID NO:151);
AACAATGCTG (SEQ ID NO:152);	ACAATGCTGC (SEQ ID NO:153);
CAATGCTGCT (SEQ ID NO:154);	AATGCTGCTT (SEQ ID NO:155);
ATGCTGCTTG (SEQ ID NO:156);	TGCTGCTTGT (SEQ ID NO:157);
GCTGCTTG TG (SEQ ID NO:158);	CTGCTTG TGC (SEQ ID NO:159);
TGCTTG TGCC (SEQ ID NO:160);	GCTTG TGCCCT (SEQ ID NO:161);
CTTG TGCCCTG (SEQ ID NO:162);	TTTG TGCCCTGG (SEQ ID NO:163);
TGTG CCTGGC (SEQ ID NO:164);	GTG CCTGGCT (SEQ ID NO:165);
TG CCTGGCTA (SEQ ID NO:166);	GCCTGGCTAG (SEQ ID NO:167);
CCTGGCTAGA (SEQ ID NO:168);	CTGGCTAGAA (SEQ ID NO:169);
TGGCTAGAAG (SEQ ID NO:170);	GGCTAGAAGC (SEQ ID NO:171);
GCTAGAAGCA (SEQ ID NO:172);	CTAGAAGCAC (SEQ ID NO:173);
TAGAAGCACA (SEQ ID NO:174);	AGAAGCACAA (SEQ ID NO:175);
GAAGCACAAAG (SEQ ID NO:176);	AAGCACAAAG (SEQ ID NO:177);
AGCACAAAGAG (SEQ ID NO:178);	GCACAAAGAGG (SEQ ID NO:179);
CACAAGAGGA (SEQ ID NO:180);	ACAAGAGGAG (SEQ ID NO:181);
CAAGAGGAGG (SEQ ID NO:182);	AAGAGGAGGA (SEQ ID NO:183);
AGAGGAGGAA (SEQ ID NO:184);	GAGGAGGAAG (SEQ ID NO:185);
AGGAGGAAGA (SEQ ID NO:186);	GGAGGAAGAG (SEQ ID NO:187);
GAGGAAGAGG (SEQ ID NO:188);	AGGAAGAGGT (SEQ ID NO:189);
GGAAGAGGTG (SEQ ID NO:190);	GAAGAGGTGG (SEQ ID NO:191);
AAGAGGTGGG (SEQ ID NO:192);	AGAGGTGGGT (SEQ ID NO:193);
GAGGTGGGTT (SEQ ID NO:194);	AGGTGGGTTT (SEQ ID NO:195);
GGTGGGTTTT (SEQ ID NO:196);	GTGGGTTTTC (SEQ ID NO:197);
TGGGTTTTTCC (SEQ ID NO:198);	GGGTTTTTCCA (SEQ ID NO:199);
GGTTTTTCCAG (SEQ ID NO:200);	GTTTTTCCAGT (SEQ ID NO:201);
TTTTTCCAGTC (SEQ ID NO:202);	TTTCCAGTCA (SEQ ID NO:203);
TTCCAGTCAC (SEQ ID NO:204);	TCCAGTCACA (SEQ ID NO:205);

00146783-00033

950606.p:\aport\jlt.HIV1.USA\217

- 217 -

CCAGTCACAC (SEQ ID NO:206) ;	CAGTCACACC (SEQ ID NO:207) ;
AGTCACACCT (SEQ ID NO:208) ;	GTCACACCTC (SEQ ID NO:209) ;
TCACACCTCA (SEQ ID NO:210) ;	CACACCTCAG (SEQ ID NO:211) ;
ACACCTCAGG (SEQ ID NO:212) ;	CACCTCAGGT (SEQ ID NO:213) ;
ACCTCAGGTA (SEQ ID NO:214) ;	CCTCAGGTAC (SEQ ID NO:215) ;
CTCAGGTACC (SEQ ID NO:216) ;	TCAGGTACCT (SEQ ID NO:217) ;
CAGGTACCTT (SEQ ID NO:218) ;	AGGTACCTTT (SEQ ID NO:219) ;
GGTACCTTTA (SEQ ID NO:220) ;	GTACCTTTAA (SEQ ID NO:221) ;
TACCTTTAAG (SEQ ID NO:222) ;	ACCTTTAAGA (SEQ ID NO:223) ;
CCTTTAAGAC (SEQ ID NO:224) ;	CTTTAAGACC (SEQ ID NO:225) ;
TTTAAGACCA (SEQ ID NO:226) ;	TTAAGACCAA (SEQ ID NO:227) ;
TAAGACCAAT (SEQ ID NO:228) ;	AAGACCAATG (SEQ ID NO:229) ;
AGACCAATGA (SEQ ID NO:230) ;	GACCAATGAC (SEQ ID NO:231) ;
ACCAATGACT (SEQ ID NO:232) ;	CCAATGACTT (SEQ ID NO:233) ;
CAATGACTTA (SEQ ID NO:234) ;	AATGACTTAC (SEQ ID NO:235) ;
ATGACTTACA (SEQ ID NO:236) ;	TGACTTACAA (SEQ ID NO:237) ;
GACTTACAAG (SEQ ID NO:238) ;	ACTTACAAGG (SEQ ID NO:239) ;
CTTACAAGGC (SEQ ID NO:240) ;	TTACAAGGCA (SEQ ID NO:241) ;
TACAAGGCAG (SEQ ID NO:242) ;	ACAAGGCAGC (SEQ ID NO:243) ;
CAAGGCAGCT (SEQ ID NO:244) ;	AAGGCAGCTG (SEQ ID NO:245) ;
AGGCAGCTGT (SEQ ID NO:246) ;	GGCAGCTGTA (SEQ ID NO:247) ;
GCAGCTGTAG (SEQ ID NO:248) ;	CAGCTGTAGA (SEQ ID NO:249) ;
AGCTGTAGAT (SEQ ID NO:250) ;	GCTGTAGATC (SEQ ID NO:251) ;
CTGTAGATCT (SEQ ID NO:252) ;	TGTAGATCTT (SEQ ID NO:253) ;
GTAGATCTTA (SEQ ID NO:254) ;	TAGATCTTAG (SEQ ID NO:255) ;
AGATCTTAGC (SEQ ID NO:256) ;	GATCTTAGCC (SEQ ID NO:257) ;
ATCTTAGCCA (SEQ ID NO:258) ;	TCTTAGCCAC (SEQ ID NO:259) ;
CTTAGCCACT (SEQ ID NO:260) ;	TTAGCCACTT (SEQ ID NO:261) ;
TAGCCACTTT (SEQ ID NO:262) ;	AGCCACTTTT (SEQ ID NO:263) ;
GCCACTTTTT (SEQ ID NO:264) ;	CCACTTTTTA (SEQ ID NO:265) ;
CACTTTTTAA (SEQ ID NO:266) ;	ACTTTTTTAA (SEQ ID NO:267) ;
CTTTTTTAAA (SEQ ID NO:268) ;	TTTTTTAAAG (SEQ ID NO:269) ;
TTTTTAAAGA (SEQ ID NO:270) ;	TTTAAAGAA (SEQ ID NO:271) ;
TTAAAGAAA (SEQ ID NO:272) ;	TAAAGAAAA (SEQ ID NO:273) ;
AAAAGAAAAG (SEQ ID NO:274) ;	AAAGAAAAGG (SEQ ID NO:275) ;
AAGAAAAGGG (SEQ ID NO:276) ;	AGAAAAGGGG (SEQ ID NO:277) ;
GAAAAGGGGG (SEQ ID NO:278) ;	AAAAGGGGGG (SEQ ID NO:279) ;
AAAGGGGGGA (SEQ ID NO:280) ;	AAGGGGGGAC (SEQ ID NO:281) ;

00145793-000399

950606.prtoper@jib.fr - USA,218

- 218 -

AGGGGGGACT (SEQ ID NO:282); GGGGGGACTG (SEQ ID NO:283);
GGGGGACTGG (SEQ ID NO:284); GGGGACTGGA (SEQ ID NO:285);
GGGACTGGAA (SEQ ID NO:286); GGACTGGAAG (SEQ ID NO:287);
GACTGGAAGG (SEQ ID NO:288); ACTGGAAGGG (SEQ ID NO:289);
CTGGAAGGGC (SEQ ID NO:290); TGAAGGGGCT (SEQ ID NO:291);
GGAAGGGGCTA (SEQ ID NO:292); GAAGGGGCTAA (SEQ ID NO:293);
AAGGGGCTAAT (SEQ ID NO:294); AGGGGCTAATT (SEQ ID NO:295);
GGGCTAATTC (SEQ ID NO:296); GGCTAATTCA (SEQ ID NO:297);
GCTAATTCAC (SEQ ID NO:298); CTAATTCACT (SEQ ID NO:299);
TAATTCACTC (SEQ ID NO:300); AATTCACTCC (SEQ ID NO:301);
ATTCACTCCC (SEQ ID NO:302); TTCACTCCCA (SEQ ID NO:303);
TCACTCCCAA (SEQ ID NO:304); CACTCCCAA (SEQ ID NO:305);
ACTCCCAAAG (SEQ ID NO:306); CTCCTCAAAGA (SEQ ID NO:307);
TCCCAAAGAA (SEQ ID NO:308); CCCAAAGAAG (SEQ ID NO:309);
CCAAAGAAGA (SEQ ID NO:310); CAAAGAAGAC (SEQ ID NO:311);
AAAGAAGACA (SEQ ID NO:312); AAGAAGACAA (SEQ ID NO:313);
AGAAGACAAG (SEQ ID NO:314); GAAGACAAGA (SEQ ID NO:315);
AAGACAAGAT (SEQ ID NO:316); AGACAAGATA (SEQ ID NO:317);
GACAAGATAT (SEQ ID NO:318); ACAAGATATC (SEQ ID NO:319);
CAAGATATCC (SEQ ID NO:320); AAGATATCCT (SEQ ID NO:321);
AGATATCCTT (SEQ ID NO:322); GATATCCTTG (SEQ ID NO:323);
ATATCCTTGA (SEQ ID NO:324); TATCCTTGAT (SEQ ID NO:325);
ATCCTTGATC (SEQ ID NO:326); TCCTTGATCT (SEQ ID NO:327);
CCTTGATCTG (SEQ ID NO:328); CTTGATCTGT (SEQ ID NO:329);
TTGATCTGTG (SEQ ID NO:330); TGATCTGTGG (SEQ ID NO:331);
GATCTGTGGA (SEQ ID NO:332); ATCTGTGGAT (SEQ ID NO:333);
TCTGTGGATC (SEQ ID NO:334); CTGTGGATCT (SEQ ID NO:335);
TGTGGATCTA (SEQ ID NO:336); GTGGATCTAC (SEQ ID NO:337);
TGGATCTACC (SEQ ID NO:338); GGATCTACCA (SEQ ID NO:339);
GATCTACCAC (SEQ ID NO:340); ATCTACCACA (SEQ ID NO:341);
TCTACCACAC (SEQ ID NO:342); CTACCACACA (SEQ ID NO:343);
TACCACACAC (SEQ ID NO:344); ACCACACACA (SEQ ID NO:345);
CCACACACAA (SEQ ID NO:346); CACACACAAG (SEQ ID NO:347);
ACACACAAGG (SEQ ID NO:348); CACACAAGGC (SEQ ID NO:349);
ACACAAGGCT (SEQ ID NO:350); CACAAGGCTA (SEQ ID NO:351);
ACAAGGCTAC (SEQ ID NO:352); CAAGGCTACT (SEQ ID NO:353);
AAGGCTACTT (SEQ ID NO:354); AGGCTACTTC (SEQ ID NO:355);
GGCTACTTCC (SEQ ID NO:356); GCTACTTCCC (SEQ ID NO:357);

00415783-090305

- 219 -

CTACTTCCCT (SEQ ID NO:358);	TACTTCCCTG (SEQ ID NO:359);
ACTTCCCTGA (SEQ ID NO:360);	CTTCCCTGAT (SEQ ID NO:361);
TTCCCTGATT (SEQ ID NO:362);	TCCCTGATTG (SEQ ID NO:363);
CCCTGATTGG (SEQ ID NO:364);	CCTGATTGGC (SEQ ID NO:365);
CTGATTGGCA (SEQ ID NO:366);	TGATTGGCAG (SEQ ID NO:367);
GATTGGCAGA (SEQ ID NO:368);	ATTGGCAGAA (SEQ ID NO:369);
TTGGCAGAAC (SEQ ID NO:370);	TGGCAGAACT (SEQ ID NO:371);
GGCAGAACTA (SEQ ID NO:372);	GCAGAACTAC (SEQ ID NO:373);
CAGAACTACA (SEQ ID NO:374);	AGAACTACAC (SEQ ID NO:375);
GAACCTACACA (SEQ ID NO:376);	AACTACACAC (SEQ ID NO:377);
ACTACACACC (SEQ ID NO:378);	CTACACACCA (SEQ ID NO:379);
TACACACCAG (SEQ ID NO:380);	ACACACCAGG (SEQ ID NO:381);
CACACCAGGG (SEQ ID NO:382);	ACACCAGGGC (SEQ ID NO:383);
CACCAGGGCC (SEQ ID NO:384);	ACCAGGGCCA (SEQ ID NO:385);
CCAGGGCCAG (SEQ ID NO:386);	CAGGGCCAGG (SEQ ID NO:387);
AGGGCCAGGG (SEQ ID NO:388);	GGGCCAGGGG (SEQ ID NO:389);
GGCCAGGGGT (SEQ ID NO:390);	GCCAGGGGTC (SEQ ID NO:391);
CCAGGGGTCA (SEQ ID NO:392);	CAGGGGTCAG (SEQ ID NO:393);
AGGGGTGAGA (SEQ ID NO:394);	GGGGTCAGAT (SEQ ID NO:395);
GGGTGAGATA (SEQ ID NO:396);	GGTCAGATAT (SEQ ID NO:397);
GTCAGATATC (SEQ ID NO:398);	TCAGATATCC (SEQ ID NO:399);
CAGATATCCA (SEQ ID NO:400);	AGATATCCAC (SEQ ID NO:401);
GATATCCACT (SEQ ID NO:402);	ATATCCACTG (SEQ ID NO:403);
TATCCACTGA (SEQ ID NO:404);	ATCCACTGAC (SEQ ID NO:405);
TCCACTGACC (SEQ ID NO:406);	CCACTGACCT (SEQ ID NO:407);
CACTGACCTT (SEQ ID NO:408);	ACTGACCTTT (SEQ ID NO:409);
CTGACCTTTG (SEQ ID NO:410);	TGACCTTTGG (SEQ ID NO:411);
GACCTTTGGA (SEQ ID NO:412);	ACCTTTGGAT (SEQ ID NO:413);
CCTTTGGATG (SEQ ID NO:414);	CTTTGGATGG (SEQ ID NO:415);
TTTGGATGGT (SEQ ID NO:416);	TTGGATGGTG (SEQ ID NO:417);
TGGATGGTGC (SEQ ID NO:418);	GGATGGTGCT (SEQ ID NO:419);
GATGGTGCTA (SEQ ID NO:420);	ATGGTGCTAC (SEQ ID NO:421);
TGGTGCTACA (SEQ ID NO:422);	GGTGCTACAA (SEQ ID NO:423);
GTGCTACAAG (SEQ ID NO:424);	TGCTACAAGC (SEQ ID NO:425);
GCTACAAGCT (SEQ ID NO:426);	CTACAAGCTA (SEQ ID NO:427);
TACAAGCTAG (SEQ ID NO:428);	ACAAGCTAGT (SEQ ID NO:429);
CAAGCTAGTA (SEQ ID NO:430);	AAGCTAGTAC (SEQ ID NO:431);
AGCTAGTACC (SEQ ID NO:432);	GCTAGTACCA (SEQ ID NO:433);

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- 220 -

CTAGTACCAG (SEQ ID NO:434); TAGTACCAGT (SEQ ID NO:435);
AGTACCAGTT (SEQ ID NO:436); GTACCAGTTG (SEQ ID NO:437);
TACCAGTTGA (SEQ ID NO:438); ACCAGTTGAG (SEQ ID NO:439);
CCAGTTGAGC (SEQ ID NO:440); CAGTTGAGCC (SEQ ID NO:441);
AGTTGAGCCA (SEQ ID NO:442); GTTGAGCCAG (SEQ ID NO:443);
TTGAGCCAGA (SEQ ID NO:444); TGAGCCAGAT (SEQ ID NO:445);
GAGCCAGATA (SEQ ID NO:446); AGCCAGATAA (SEQ ID NO:447);
GCCAGATAAG (SEQ ID NO:448); CCAGATAAGG (SEQ ID NO:449);
CAGATAAGGT (SEQ ID NO:450); AGATAAGGTA (SEQ ID NO:451);
GATAAGGTAG (SEQ ID NO:452); ATAAGGTAGA (SEQ ID NO:453);
TAAGGTAGAA (SEQ ID NO:454); AAGGTAGAAG (SEQ ID NO:455);
AGGTAGAAGA (SEQ ID NO:456); GGTAGAAGAG (SEQ ID NO:457);
GTAGAAGAGG (SEQ ID NO:458); TAGAAGAGGC (SEQ ID NO:459);
AGAAGAGGCC (SEQ ID NO:460); GAAGAGGCCA (SEQ ID NO:461);
AAGAGGCCAA (SEQ ID NO:462); AGAGGCCAAT (SEQ ID NO:463);
GAGGCCAATA (SEQ ID NO:464); AGGCCAATAA (SEQ ID NO:465);
GGCCAATAAA (SEQ ID NO:466); GCCAATAAAG (SEQ ID NO:467);
CCAATAAAGG (SEQ ID NO:468); CAATAAAGGA (SEQ ID NO:469);
AATAAAGGAG (SEQ ID NO:470); ATAAAGGAGA (SEQ ID NO:471);
TAAAGGAGAG (SEQ ID NO:472); AAAGGAGAGA (SEQ ID NO:473);
AAGGAGAGAA (SEQ ID NO:474); AGGAGAGAAC (SEQ ID NO:475);
GGAGAGAACA (SEQ ID NO:476); GAGAGAACAC (SEQ ID NO:477);
AGAGAACACC (SEQ ID NO:478); GAGAACACCA (SEQ ID NO:479);
AGAACACCAG (SEQ ID NO:480); GAACACCAGC (SEQ ID NO:481);
AACACCAGCT (SEQ ID NO:482); ACACCAGCTT (SEQ ID NO:483);
CACCAGCTTG (SEQ ID NO:484); ACCAGCTTGT (SEQ ID NO:485);
CCAGCTTGTT (SEQ ID NO:486); CAGCTTGTTA (SEQ ID NO:487);
AGCTTGTTAC (SEQ ID NO:488); GCTTGTTACA (SEQ ID NO:489);
CTTGTTACAC (SEQ ID NO:490); TTGTTACACC (SEQ ID NO:491);
TGTTACACCC (SEQ ID NO:492); GTTACACCCT (SEQ ID NO:493);
TTACACCCTG (SEQ ID NO:494); TACACCCTGT (SEQ ID NO:495);
ACACCCTGTG (SEQ ID NO:496); CACCCTGTGA (SEQ ID NO:497);
ACCCTGTGAG (SEQ ID NO:498); CCCTGTGAGC (SEQ ID NO:499);
CCTGTGAGCC (SEQ ID NO:500); CTGTGAGCCT (SEQ ID NO:501);
TGTGAGCCTG (SEQ ID NO:502); GTGAGCCTGC (SEQ ID NO:503);
TGAGCCTGCA (SEQ ID NO:504); GAGCCTGCAT (SEQ ID NO:505);
AGCCTGCATG (SEQ ID NO:506); GCCTGCATGG (SEQ ID NO:507);
CCTGCATGGA (SEQ ID NO:508); CTGCATGGAA (SEQ ID NO:509);

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- 221 -

TGCATGGAAT (SEQ ID NO:510); GCATGGAATG (SEQ ID NO:511);
CATGGAATGG (SEQ ID NO:512); ATGGAATGGA (SEQ ID NO:513);
TGGAATGGAT (SEQ ID NO:514); GGAATGGATG (SEQ ID NO:515);
GAATGGATGA (SEQ ID NO:516); AATGGATGAC (SEQ ID NO:517);
ATGGATGACC (SEQ ID NO:518); TGGATGACCC (SEQ ID NO:519);
GGATGACCCT (SEQ ID NO:520); GATGACCCTG (SEQ ID NO:521);
ATGACCCTGA (SEQ ID NO:522); TGACCCTGAG (SEQ ID NO:523);
GACCCTGAGA (SEQ ID NO:524); ACCCTGAGAG (SEQ ID NO:525);
CCCTGAGAGA (SEQ ID NO:526); CCTGAGAGAG (SEQ ID NO:527);
CTGAGAGAGA (SEQ ID NO:528); TGAGAGAGAA (SEQ ID NO:529);
GAGAGAGAAG (SEQ ID NO:530); AGAGAGAAGT (SEQ ID NO:531);
GAGAGAAGTG (SEQ ID NO:532); AGAGAAGTGT (SEQ ID NO:533);
GAGAAGTGTT (SEQ ID NO:534); AGAAGTGTTA (SEQ ID NO:535);
GAAGTGTTAG (SEQ ID NO:536); AAGTGTTAGA (SEQ ID NO:537);
AGTGTTAGAG (SEQ ID NO:538); GTGTTAGAGT (SEQ ID NO:539);
TGTTAGAGTG (SEQ ID NO:540); GTTAGAGTGG (SEQ ID NO:541);
TTAGAGTGGA (SEQ ID NO:542); TAGAGTGGAG (SEQ ID NO:543);
AGAGTGGAGG (SEQ ID NO:544); GAGTGGAGGT (SEQ ID NO:545);
AGTGGAGGTT (SEQ ID NO:546); GTGGAGGTTT (SEQ ID NO:547);
TGGAGGTTTG (SEQ ID NO:548); GGAGGTTTGA (SEQ ID NO:549);
GAGGTTTGAC (SEQ ID NO:550); AGGTTTGACA (SEQ ID NO:551);
GGTTTGACAG (SEQ ID NO:552); GTTTGACAGC (SEQ ID NO:553);
TTTGACAGCC (SEQ ID NO:554); TTGACAGCCG (SEQ ID NO:555);
TGACAGCCGC (SEQ ID NO:556); GACAGCCGCC (SEQ ID NO:557);
ACAGCCGCCT (SEQ ID NO:558); CAGCCGCCTA (SEQ ID NO:559);
AGCCGCCTAG (SEQ ID NO:560); GCCGCCTAGC (SEQ ID NO:561);
CCGCCTAGCA (SEQ ID NO:562); CGCCTAGCAT (SEQ ID NO:563);
GCCTAGCATT (SEQ ID NO:564); CCTAGCATTT (SEQ ID NO:565);
CTAGCATTTT (SEQ ID NO:566); TAGCATTTCA (SEQ ID NO:567);
AGCATTTTCAT (SEQ ID NO:568); GCATTTTCATC (SEQ ID NO:569);
CATTTTCATCA (SEQ ID NO:570); ATTTTCATCAC (SEQ ID NO:571);
TTTCATCACG (SEQ ID NO:572); TTCATCACGT (SEQ ID NO:573);
TCATCACGTG (SEQ ID NO:574); CATCACGTGG (SEQ ID NO:575);
ATCACGTGGC (SEQ ID NO:576); TCACGTGGCC (SEQ ID NO:577);
CACGTGGCCC (SEQ ID NO:578); ACGTGGCCCC (SEQ ID NO:579);
CGTGGCCCCG (SEQ ID NO:580); GTGGCCCCGAG (SEQ ID NO:581);
TGGCCCCGAGA (SEQ ID NO:582); GGCCCCGAGAG (SEQ ID NO:583);
GCCCCGAGAGC (SEQ ID NO:584); CCCGAGAGCT (SEQ ID NO:585);

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930606, p10p0r1cjh, HIV1.L, 222

- 222 -

CCGAGAGCTG (SEQ ID NO:586);	CGAGAGCTGC (SEQ ID NO:587);
GAGAGCTGCA (SEQ ID NO:588);	AGAGCTGCAT (SEQ ID NO:589);
GAGCTGCATC (SEQ ID NO:590);	AGCTGCATCC (SEQ ID NO:591);
GCTGCATCCG (SEQ ID NO:592);	CTGCATCCGG (SEQ ID NO:593);
TGCATCCGGA (SEQ ID NO:594);	GCATCCGGAG (SEQ ID NO:595);
CATCCGGAGT (SEQ ID NO:596);	ATCCGGAGTA (SEQ ID NO:597);
TCCGGAGTAC (SEQ ID NO:598);	CCGGAGTACT (SEQ ID NO:599);
CGGAGTACTT (SEQ ID NO:600);	GGAGTACTTC (SEQ ID NO:601);
GAGTACTTCA (SEQ ID NO:602);	AGTACTTCAA (SEQ ID NO:603);
GTACTTCAAG (SEQ ID NO:604);	TACTTCAAGA (SEQ ID NO:605);
ACTTCAAGAA (SEQ ID NO:606);	CTTCAAGAAC (SEQ ID NO:607);
TTCAAGAACT (SEQ ID NO:608);	TCAAGAACTG (SEQ ID NO:609);
CAAGAACTGC (SEQ ID NO:610);	AAGAACTGCT (SEQ ID NO:611);
AGAAGCTGCTG (SEQ ID NO:612);	GAACTGCTGA (SEQ ID NO:613).

15. A strain of HIV-1 according to claim 14 wherein said deletion encompasses at least one of the following decanucleotide deletions from the *nef* gene:

ACCAGCTTGT [SEQ ID NO:803]	CCAGCTTGTT [SEQ ID NO:804]
CAGCTTGTTA [SEQ ID NO:805]	AGCTTGTTAC [SEQ ID NO:806]
GCTTGTTACA [SEQ ID NO:807]	CTTGTTACAC [SEQ ID NO:808]
TTGTTACACC [SEQ ID NO:809]	TGTTACACCC [SEQ ID NO:810]
GTTACACCCT [SEQ ID NO:811]	TTACACCCTG [SEQ ID NO:812]
TACACCCTGT [SEQ ID NO:813]	ACACCCTGTG [SEQ ID NO:814]
CACCCTGTGA [SEQ ID NO:815]	ACCCTGTGAG [SEQ ID NO:816]
CCCTGTGAGC [SEQ ID NO:817]	CCTGTGAGCC [SEQ ID NO:818]
CTGTGAGCCT [SEQ ID NO:819]	TGTGAGCCTG [SEQ ID NO:820]
GTGAGCCTGC [SEQ ID NO:821]	TGAGCCTGCA [SEQ ID NO:822]
GAGCCTGCAT [SEQ ID NO:823]	AGCCTGCATG [SEQ ID NO:824]
GCCTGCATGG [SEQ ID NO:825]	CCTGCATGGA [SEQ ID NO:826]
CTGCATGGAA [SEQ ID NO:827]	TGCATGGAAT [SEQ ID NO:828]
GCATGGAATG [SEQ ID NO:829]	CATGGAATGG [SEQ ID NO:830]
ATGGAATGGA [SEQ ID NO:831]	TGGAATGGAT [SEQ ID NO:832]
GGAATGGATG [SEQ ID NO:833]	GAATGGATGA [SEQ ID NO:834]
AATGGATGAC [SEQ ID NO:835]	ATGGATGACC [SEQ ID NO:836]
TGGATGACCC [SEQ ID NO:837]	GGATGACCCT [SEQ ID NO:838]
GATGACCCTG [SEQ ID NO:839]	ATGACCCTGA [SEQ ID NO:840]
TGACCCTGAG [SEQ ID NO:841]	

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- 223 -

16. A strain of HIV-1 according to claim 8 wherein said deletion encompasses at least one of the following decanucleotides from the LTR region of HIV-1_{NL43}:

GCTTTTGGCC	(SEQ ID NO:652);	CTTTTGCCT	(SEQ ID NO:653);
TTTTTGCCTG	(SEQ ID NO:654);	TTTGCCTGT	(SEQ ID NO:655);
TTTGCCTGTA	(SEQ ID NO:656);	TGCTGTAC	(SEQ ID NO:657);
TGCTGTACT	(SEQ ID NO:658);	GCCTGTACTG	(SEQ ID NO:659);
CCTGTACTGG	(SEQ ID NO:660);	CTGTACTGGG	(SEQ ID NO:661);
TGTACTGGGT	(SEQ ID NO:662);	GTACTGGGTC	(SEQ ID NO:663);
TACTGGGTCT	(SEQ ID NO:664);	ACTGGGTCTC	(SEQ ID NO:665);
CTGGGTCTCT	(SEQ ID NO:666);	TGGGTCTCTC	(SEQ ID NO:667);
GGGTCTCTCT	(SEQ ID NO:668);	GGTCTCTCTG	(SEQ ID NO:669);
GTCTCTCTGG	(SEQ ID NO:670);	TCTCTCTGGT	(SEQ ID NO:671);
CTCTCTGGTT	(SEQ ID NO:672);	TCTCTGGTTA	(SEQ ID NO:673);
CTCTGGTTAG	(SEQ ID NO:674);	TCTCTGGTTA	(SEQ ID NO:675);
CTGGTTAGAC	(SEQ ID NO:676);	TGGTTAGACC	(SEQ ID NO:677);
GGTTAGACCA	(SEQ ID NO:678);	GTTAGACCAG	(SEQ ID NO:679);
TTAGACCAGA	(SEQ ID NO:680);	TAGACCAGAT	(SEQ ID NO:681);
AGACCAGATC	(SEQ ID NO:682);	GACCAGATCT	(SEQ ID NO:683);
ACCAGATCTG	(SEQ ID NO:684);	CCAGATCTGA	(SEQ ID NO:685);
CAGATCTGAG	(SEQ ID NO:686);	AGATCTGAGC	(SEQ ID NO:687);
GATCTGAGCC	(SEQ ID NO:688);	ATCTGAGCCT	(SEQ ID NO:689);
TCTGAGCCTG	(SEQ ID NO:690);	CTGAGCCTGG	(SEQ ID NO:691);
TGAGCCTGGG	(SEQ ID NO:692);	GAGCCTGGGA	(SEQ ID NO:693);
AGCCTGGGAG	(SEQ ID NO:694);	GCCTGGGAGC	(SEQ ID NO:695);
CCTGGGAGCT	(SEQ ID NO:696);	CTGGGAGCTC	(SEQ ID NO:697);
TGGGAGCTCT	(SEQ ID NO:698);	GGGAGCTCTC	(SEQ ID NO:699);
GGAGCTCTCT	(SEQ ID NO:700);	GAGCTCTCTG	(SEQ ID NO:701);
AGCTCTCTGG	(SEQ ID NO:702);	GCTCTCTGGC	(SEQ ID NO:703);
CTCTCTGGCT	(SEQ ID NO:704);	TCTCTGGCTA	(SEQ ID NO:705);
CTCTGGCTAA	(SEQ ID NO:706);	TCTGGCTAAC	(SEQ ID NO:707);
CTGGCTAACT	(SEQ ID NO:708);	TGGCTAACTA	(SEQ ID NO:709);
GGCTAACTAG	(SEQ ID NO:710);	GCTAACTAGG	(SEQ ID NO:711);
CTAACTAGGG	(SEQ ID NO:712);	TAACTAGGGA	(SEQ ID NO:713);
AACTAGGGAA	(SEQ ID NO:714);	ACTAGGGAAC	(SEQ ID NO:715);
CTAGGGAAACC	(SEQ ID NO:716);	TAGGGAAACC	(SEQ ID NO:717);
AGGGAAACCA	(SEQ ID NO:718);	GGGAACCCAC	(SEQ ID NO:719);
GGAACCCACT	(SEQ ID NO:720);	GAACCCACTG	(SEQ ID NO:721);

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- 224 -

AACCCACTGC (SEQ ID NO:722); ACCCACTGCT (SEQ ID NO:723);
CCCACTGCTT (SEQ ID NO:724); CCACTGCTTA (SEQ ID NO:725);
CACTGCTTAA (SEQ ID NO:726); ACTGCTTAAG (SEQ ID NO:727);
CTGCTTAAGC (SEQ ID NO:728); TGCTTAAGCC (SEQ ID NO:729);
GCTTAAGCCT (SEQ ID NO:730); CTTAAGCCTC (SEQ ID NO:731);
TTAAGCCTCA (SEQ ID NO:732); TAAGCCTCAA (SEQ ID NO:733);
AAGCCTCAAT (SEQ ID NO:734); AGCCTCAATA (SEQ ID NO:735);
GCCTCAATAA (SEQ ID NO:736); CCTCAATAAA (SEQ ID NO:737);
CTCAATAAAG (SEQ ID NO:738); TCAATAAAGC (SEQ ID NO:739);
CAATAAAGCT (SEQ ID NO:740); AATAAAGCTT (SEQ ID NO:741);
ATAAAGCTTG (SEQ ID NO:742); TAAAGCTTGC (SEQ ID NO:743);
AAAGCTTGCC (SEQ ID NO:744); AAGCTTGCCCT (SEQ ID NO:745);
AGCTTGCCCT (SEQ ID NO:746); GCTTGCCCTG (SEQ ID NO:747);
CTTGCCCTGA (SEQ ID NO:748); TTGCCTTGAG (SEQ ID NO:749);
TGCCCTGAGT (SEQ ID NO:750); GCCTTGAGTG (SEQ ID NO:751);
CCTTGAGTGC (SEQ ID NO:752); CTTGAGTGCT (SEQ ID NO:753);
TTGAGTGCTT (SEQ ID NO:754); TGAGTGCTTC (SEQ ID NO:755);
GAGTGCTTCA (SEQ ID NO:756); AGTGCTTCAA (SEQ ID NO:757);
GTGCTTCAAG (SEQ ID NO:758); TGCTTCAAGT (SEQ ID NO:759);
GCTTCAAGTA (SEQ ID NO:760); CTTCAAGTAG (SEQ ID NO:761);
TTCAAGTAGT (SEQ ID NO:762); TCAAGTAGTG (SEQ ID NO:763);
CAAGTAGTGT (SEQ ID NO:764); AAGTAGTGTG (SEQ ID NO:765);
AGTAGTGTGT (SEQ ID NO:766); GTAGTGTGTG (SEQ ID NO:767);
TAGTGTGTGC (SEQ ID NO:768); AGTGTGTGCC (SEQ ID NO:769);
GTGTGTGCCC (SEQ ID NO:770); TGTGTGCCCCG (SEQ ID NO:771);
GTGTGCCCCGT (SEQ ID NO:772); TGTGCCCCGTC (SEQ ID NO:773);
GTGCCCCGTCT (SEQ ID NO:774); TGCCCCGTCTG (SEQ ID NO:775);
GCCCCGTCTGT (SEQ ID NO:776); CCGCTCTGTT (SEQ ID NO:777);
CCGTCTGTTG (SEQ ID NO:778); CGTCTGTTGT (SEQ ID NO:779);
GTCTGTTGTG (SEQ ID NO:780); TCTGTTGTGT (SEQ ID NO:781);
CTGTTGTGTG (SEQ ID NO:782); TGTGTTGTGA (SEQ ID NO:783);
GTTGTGTGAC (SEQ ID NO:784); TTGTGTGACT (SEQ ID NO:785);
TGTGTGACTC (SEQ ID NO:786); GTGTGACTCT (SEQ ID NO:787);
TGTGTGACTC (SEQ ID NO:788); GTGTGACTCT (SEQ ID NO:789);
TGTGACTCTG (SEQ ID NO:790); GTGACTCTGG (SEQ ID NO:791);
TGACTCTGGT (SEQ ID NO:792); GACTCTGGTA (SEQ ID NO:793);
ACTCTGGTAA (SEQ ID NO:794); CTCCTGGTAAC (SEQ ID NO:795);
TCTGGTAACT (SEQ ID NO:796); CTGGTAACTA (SEQ ID NO:797);

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- 225 -

TGGTAACTAG (SEQ ID NO:798); GGTAAC TAGA (SEQ ID NO:799).

17. An isolated strain of HIV-1 or a biological source thereof, said HIV-1 having the following characteristics:

- (i) is substantially non-pathogenic in human subjects; and
- (ii) carries a modified *nef* gene which encodes a *nef* gene product substantially immunologically non-interactive with antibodies to amino acids 162 to 177 of Nef in wild-type HIV-1.

18. An isolated strain of HIV-1 according to claim 17 wherein said *nef* gene product is interactive with antibodies to wild-type HIV-1 Nef but is substantially non-interactive with antibodies to amino acids 162 to 177 of wild-type HIV-1 Nef protein.

19. An isolated strain of HIV-1 according to claim 17 comprising a mutation in its genome such that amino acids 162 to 177 of wild-type HIV-1 Nef are substantially not represented in a Nef protein or derivative thereof produced by said isolated HIV-1 strain, or are represented in an amount insufficient to induce an immune response to that region of Nef.

20. An isolated strain of HIV-1 according to claim 17 wherein said strain of HIV-1 carries a mutation in one or more of nucleotides 9271 to 9317 of HIV-1_{NL43} or in a functionally equivalent region in another pathogenic strain of HIV-1.

21. An isolated non-pathogenic strain of HIV-1 comprising a genome which is substantially incapable of hybridizing under medium stringent conditions to a nucleic acid molecule comprising a sequence of nucleotides which encodes all or part of amino acids 162 to 177 of wild-type HIV-1 Nef.

22. A non-pathogenic HIV-1 isolate which:

- (i) induces an immune response in a human or primate subject;
- (ii) does not substantially produce a proliferative response or cytokine production to a mitogen, alloantigen and/or recall antigen relative to a healthy, non-infected subject; and

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- 226 -

- (iii) is substantially incapable of inducing an antibody response to amino acids 162 to 177 of wild-type HIV-1 Nef protein.

23. A viral isolate which:

- (i) is interactive to antibodies to a glycoprotein from HIV-1 selected from gp41-45, gp120 and gp160;
- (ii) is substantially non-pathogenic in human subjects; and
- (iii) carries a deletion mutation of at least ten nucleotides in a region corresponding to all or part of amino acids 162 to 177 encoded by the *nef* gene of a pathogenic strain of HIV-1.

24. A viral isolate which:

- (i) is reactive to antibodies to a glycoprotein from HIV-1 selected from gp41-45, gp120 and gp160;
- (ii) carries a deletion of at least ten nucleotides in a region corresponding to the *nef* gene in HIV-1_{NL43}; and

wherein said deletion encompasses one or more of the following deca-nucleotides from the *nef* gene of HIV-1_{NL43} or corresponding sequences from another pathogenic strain of HIV-1:

ACCAGCTTGT [SEQ ID NO:4]	CCAGCTTGTT [SEQ ID NO:5]
CAGCTTGTTA [SEQ ID NO:6]	AGCTTGTTAC [SEQ ID NO:7]
GCTTGTTACA [SEQ ID NO:8]	CTTGTTACAC [SEQ ID NO:9]
TTGTTACACC [SEQ ID NO:10]	TGTTACACCC [SEQ ID NO:11]
GTTACACCCT [SEQ ID NO:12]	TTACACCCTG [SEQ ID NO:13]
TACACCCTGT [SEQ ID NO:14]	ACACCCTGTG [SEQ ID NO:15]
CACCCTGTGA [SEQ ID NO:16]	ACCCTGTGAG [SEQ ID NO:17]
CCCTGTGAGC [SEQ ID NO:18]	CCTGTGAGCC [SEQ ID NO:19]
CTGTGAGCCT [SEQ ID NO:20]	TGTGAGCCTG [SEQ ID NO:21]
GTGAGCCTGC [SEQ ID NO:22]	TGAGCCTGCA [SEQ ID NO:23]
GAGCCTGCAT [SEQ ID NO:24]	AGCCTGCATG [SEQ ID NO:25]
GCCTGCATGG [SEQ ID NO:26]	CCTGCATGGA [SEQ ID NO:27]
CTGCATGGAA [SEQ ID NO:28]	TGCATGGAAT [SEQ ID NO:29]
GCATGGAATG [SEQ ID NO:30]	CATGGAATGG [SEQ ID NO:31]
ATGGAATGGA [SEQ ID NO:32]	TGGAATGGAT [SEQ ID NO:33]
GGAATGGATG [SEQ ID NO:34]	GAATGGATGA [SEQ ID NO:35]

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- 227 -

AATGGATGAC [SEQ ID NO:36]	ATGGATGACC [SEQ ID NO:37]
TGGATGACCC [SEQ ID NO:38]	GGATGACCCT [SEQ ID NO:39]
GATGACCCTG [SEQ ID NO:40]	ATGACCCTGA [SEQ ID NO:41]
TGACCCTGAG [SEQ ID NO:42]	

25. An isolated strain of HIV-1 having the identifying characteristics of HIV-1 isolate ECACC Accession No. V94101706 or HIV-1 isolate ECACC Accession No. V941031169 or ECACC Accession N. V95031022.
26. An isolated strain of HIV-1 which is reactive to antibodies to a glycoprotein of HIV-1, is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env* and which is incapable of directing synthesis of a *nef* gene product or a full length *nef* gene product.
27. An isolated strain of HIV-1 according to claim 26 wherein the glycoprotein is at least one of gp41-45, gp120 and/or gp160.
28. A nucleic acid molecule or a part, fragment or derivative thereof from an HIV-1 isolate defined in any one of claims 1 to 26.
29. A molecular infectious clone comprising a nucleic acid molecule according to claim 28.
30. A method for inhibiting or reducing productive infection of an individual by a pathogenic strain of HIV-1, said method comprising administering to a subject a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate target cells carrying DNA derived from said non-pathogenic HIV-1.
31. A method according to claim 30 wherein said isolate is capable of stimulating an immune response in a human or primate against at least one glycoprotein on HIV-1 whilst not substantially reducing proliferative responses and cytokine production to a mitogen in said human or primate compared to a healthy, non-infected human or primate subject.

09146783-EB294T60

- 228 -

32. A method according to claim 31 wherein said isolate carries one or more mutations in its genome resulting in the inability to direct synthesis of at least one polypeptide or protein from a pathogenic strain of HIV-1.

33. A method according to claim 31 wherein said isolate carries one or more mutations in its genome resulting in said genome directing synthesis of a truncated form of a polypeptide or protein from a pathogenic strain of HIV-1.

34. A method according to claim 32 or 33 wherein said HIV-1 isolate carries a mutation in its *nef* gene and/or long terminal repeat (LTR) region or in a functionally equivalent location in the HIV-1 genome.

35. A method according to claim 34 wherein said HIV-1 isolate is interactive to antibodies to gp41-45, gp120 and/or gp160 of HIV-1 and carries a deletion of at least ten contiguous nucleotides in a region corresponding to the *nef* gene and/or LTR region of pathogenic HIV-1.

36. A method according to claim 35 wherein said HIV-1 isolate encodes a modified Nef protein without amino acids 162 to 177 of wild-type HIV-1_{NL43} Nef.

37. A method according to claim 35 or 34 wherein said HIV-1 isolate is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env*.

38. A method according to claim 37 wherein said HIV-1 isolate carries a deletion in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43}.

39. A method according to claim 38 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

- | | | |
|------------|-------|----------------|
| nucleotide | (i) | 8830-8862; |
| | (ii) | 9009-9035; |
| | (iii) | 9019-9029; and |

0014573-090369

950606.p4epcr/hh,HIV1.US.229

- 229 -

(iv) 9033-9049.

40. A method according to claim 38 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(v)	9281-9371;
	(vi)	9281-9362;
	(vii)	9105-9224; and
	(viii)	9271-9370.

41. A method according to claim 38 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(ix)	8882-8928;
	(x)	8850-9006;
	(xi)	8792-9041; and
	(xii)	9112-9204.

42. A method according to claim 38 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(xiii)	9105-9224;
	(xiv)	9389-9395; and
	(xv)	9281-9366.

43. A method according to claim 38 wherein said deletion encompasses at least one of the following decanucleotides from the nef gene of HIV-1_{NL43}:

ATGGGTGGCA (SEQ ID NO:2);	TGGGTGGCAA (SEQ ID NO:3);
GGGTGGCAAG (SEQ ID NO:4);	GGTGGCAAGT (SEQ ID NO:5);
GTGGCAAGTG (SEQ ID NO:6);	TGGCAAGTGG (SEQ ID NO:7);
GGCAAGTGGT (SEQ ID NO:8);	GCAAGTGGTC (SEQ ID NO:9);
CAAGTGGTCA (SEQ ID NO:10);	AAGTGGTCAA (SEQ ID NO:11);
AGTGGTCAAA (SEQ ID NO:12);	GTGGTCAAAA (SEQ ID NO:13);
TGGTCAAAAA (SEQ ID NO:14);	GGTCAAAAAG (SEQ ID NO:15);
GTCAAAAAGT (SEQ ID NO:16);	TCAAAAAGTA (SEQ ID NO:17);
CAAAAAGTAG (SEQ ID NO:18);	AAAAAGTAGT (SEQ ID NO:19);
AAAAGTAGTG (SEQ ID NO:20);	AAAGTAGTGT (SEQ ID NO:21);

86E050-E8294T60

- 230 -

AAGTAGTGTG (SEQ ID NO:22);	AGTAGTGTGA (SEQ ID NO:23);
GTAGTGTGAT (SEQ ID NO:24);	TAGTGTGATT (SEQ ID NO:25);
AGTGTGATTG (SEQ ID NO:26);	GTGTGATTGG (SEQ ID NO:27);
TGTGATTGGA (SEQ ID NO:28);	GTGATTGGAT (SEQ ID NO:29);
TGATTGGATG (SEQ ID NO:30);	GATTGGATGG (SEQ ID NO:31);
ATTGGATGGC (SEQ ID NO:32);	TTGGATGGCC (SEQ ID NO:33);
TGGATGGCCT (SEQ ID NO:34);	GGATGGCCTG (SEQ ID NO:35);
GATGGCCTGC (SEQ ID NO:36);	ATGGCCTGCT (SEQ ID NO:37);
TGGCCTGCTG (SEQ ID NO:38);	GGCCTGCTGT (SEQ ID NO:39);
GCCTGCTGTA (SEQ ID NO:40);	CCTGCTGTAA (SEQ ID NO:41);
CTGCTGTAAAG (SEQ ID NO:42);	TGCTGTAAAGG (SEQ ID NO:43);
GCTGTAAAGGG (SEQ ID NO:44);	CTGTAAAGGA (SEQ ID NO:45);
TGTAAGGGAA (SEQ ID NO:46);	GTAAGGGAAA (SEQ ID NO:47);
TAAGGGAAAG (SEQ ID NO:48);	AAGGGAAAGA (SEQ ID NO:49);
AGGGAAAGAA (SEQ ID NO:50);	GGGAAAGAAT (SEQ ID NO:51);
GGAAAGAATG (SEQ ID NO:52);	GAAAGAATGA (SEQ ID NO:53);
AAAGAATGAG (SEQ ID NO:54);	AAGAATGAGA (SEQ ID NO:55);
AGAATGAGAC (SEQ ID NO:56);	GAATGAGACG (SEQ ID NO:57);
AATGAGACGA (SEQ ID NO:58);	ATGAGACGAG (SEQ ID NO:59);
TGAGACGAGC (SEQ ID NO:60);	GAGACGAGCT (SEQ ID NO:61);
AGACGAGCTG (SEQ ID NO:62);	GACGAGCTGA (SEQ ID NO:63);
ACGAGCTGAG (SEQ ID NO:64);	CGAGCTGAGC (SEQ ID NO:65);
GAGCTGAGCC (SEQ ID NO:66);	AGCTGAGCCA (SEQ ID NO:67);
GCTGAGCCAG (SEQ ID NO:68);	CTGAGCCAGC (SEQ ID NO:69);
TGAGCCAGCA (SEQ ID NO:70);	GAGCCAGCAG (SEQ ID NO:71);
AGCCAGCAGC (SEQ ID NO:72);	GCCAGCAGCA (SEQ ID NO:73);
CCAGCAGCAG (SEQ ID NO:74);	CAGCAGCAGA (SEQ ID NO:75);
AGCAGCAGAT (SEQ ID NO:76);	GCAGCAGATG (SEQ ID NO:77);
CAGCAGATGG (SEQ ID NO:78);	AGCAGATGGG (SEQ ID NO:79);
GCAGATGGGG (SEQ ID NO:80);	CAGATGGGGT (SEQ ID NO:81);
AGATGGGGTG (SEQ ID NO:82);	GATGGGGTGG (SEQ ID NO:83);
ATGGGGTGGG (SEQ ID NO:84);	TGGGGTGGGA (SEQ ID NO:85);
GGGGTGGGAG (SEQ ID NO:86);	GGGTGGGAGC (SEQ ID NO:87);
GGTGGGAGCA (SEQ ID NO:88);	GTGGGAGCAG (SEQ ID NO:89);
TGGGAGCAGT (SEQ ID NO:90);	GGGAGCAGTA (SEQ ID NO:91);
GGAGCAGTAT (SEQ ID NO:92);	GAGCAGTATC (SEQ ID NO:93);
AGCAGTATCT (SEQ ID NO:94);	GCAGTATCTC (SEQ ID NO:95);
CAGTATCTCG (SEQ ID NO:96);	AGTATCTCGA (SEQ ID NO:97);

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GTATCTCGAG (SEQ ID NO:98);	TATCTCGAGA (SEQ ID NO:99);
ATCTCGAGAC (SEQ ID NO:100);	TCTCGAGACC (SEQ ID NO:101);
CTCGAGACCT (SEQ ID NO:102);	TCGAGACCTA (SEQ ID NO:103);
CGAGACCTAG (SEQ ID NO:104);	GAGACCTAGA (SEQ ID NO:105);
AGACCTAGAA (SEQ ID NO:106);	GACCTAGAAA (SEQ ID NO:107);
ACCTAGAAAA (SEQ ID NO:108);	CCTAGAAAAA (SEQ ID NO:109);
CTAGAAAAAC (SEQ ID NO:110);	TAGAAAAACA (SEQ ID NO:111);
AGAAAAACAT (SEQ ID NO:112);	GAAAAACATG (SEQ ID NO:113);
AAAAACATGG (SEQ ID NO:114);	AAACATGGA (SEQ ID NO:115);
AAACATGGAG (SEQ ID NO:116);	AACATGGAGC (SEQ ID NO:117);
ACATGGAGCA (SEQ ID NO:118);	CATGGAGCAA (SEQ ID NO:119);
ATGGAGCAAT (SEQ ID NO:120);	TGGAGCAATC (SEQ ID NO:121);
GGAGCAATCA (SEQ ID NO:122);	GAGCAATCAC (SEQ ID NO:123);
AGCAATCACA (SEQ ID NO:124);	GCAATCACAA (SEQ ID NO:125);
CAATCACAAG (SEQ ID NO:126);	AATCACAAGT (SEQ ID NO:127);
ATCACAAGTA (SEQ ID NO:128);	TCACAAGTAG (SEQ ID NO:129);
CACAAGTAGC (SEQ ID NO:130);	ACAAGTAGCA (SEQ ID NO:131);
CAAGTAGCAA (SEQ ID NO:132);	AAGTAGCAAT (SEQ ID NO:133);
AGTAGCAATA (SEQ ID NO:134);	GTAGCAATAC (SEQ ID NO:135);
TAGCAATACA (SEQ ID NO:136);	AGCAATACAG (SEQ ID NO:137);
GCAATACAGC (SEQ ID NO:138);	CAATACAGCA (SEQ ID NO:139);
AATACAGCAG (SEQ ID NO:140);	ATACAGCAGC (SEQ ID NO:141);
TACAGCAGCT (SEQ ID NO:142);	ACAGCAGCTA (SEQ ID NO:143);
CAGCAGCTAA (SEQ ID NO:144);	AGCAGCTAAC (SEQ ID NO:145);
GCAGCTAACA (SEQ ID NO:146);	CAGCTAACAA (SEQ ID NO:147);
AGCTAACAAT (SEQ ID NO:148);	GCTAACAATG (SEQ ID NO:149);
CTAACAATGC (SEQ ID NO:150);	TAACAATGCT (SEQ ID NO:151);
AACAATGCTG (SEQ ID NO:152);	ACAATGCTGC (SEQ ID NO:153);
CAATGCTGCT (SEQ ID NO:154);	AATGCTGCTT (SEQ ID NO:155);
ATGCTGCTTG (SEQ ID NO:156);	TGCTGCTTGT (SEQ ID NO:157);
GCTGCTTGTG (SEQ ID NO:158);	CTGCTTGTGC (SEQ ID NO:159);
TGCTTGTGCC (SEQ ID NO:160);	GCTTGTGCCT (SEQ ID NO:161);
CTTGTGCCTG (SEQ ID NO:162);	TTGTGCCTGG (SEQ ID NO:163);
TGTGCCTGGC (SEQ ID NO:164);	GTGCCTGGCT (SEQ ID NO:165);
TGCCTGGCTA (SEQ ID NO:166);	GCCTGGCTAG (SEQ ID NO:167);
CCTGGCTAGA (SEQ ID NO:168);	CTGGCTAGAA (SEQ ID NO:169);
TGGCTAGAAG (SEQ ID NO:170);	GGCTAGAAGC (SEQ ID NO:171);
GCTAGAAGCA (SEQ ID NO:172);	CTAGAAGCAC (SEQ ID NO:173);

- 232 -

TAGAACGACA (SEQ ID NO:174);	AGAAGCACAA (SEQ ID NO:175);
GAAGCACAAG (SEQ ID NO:176);	AAGCACAAGA (SEQ ID NO:177);
AGCACAAGAG (SEQ ID NO:178);	GCACAAGAGG (SEQ ID NO:179);
CACAAGAGGA (SEQ ID NO:180);	ACAAGAGGAG (SEQ ID NO:181);
CAAGAGGAGG (SEQ ID NO:182);	AAGAGGAGGA (SEQ ID NO:183);
AGAGGAGGAA (SEQ ID NO:184);	GAGGAGGAAAG (SEQ ID NO:185);
AGGAGGAAGA (SEQ ID NO:186);	GGAGGAAGAG (SEQ ID NO:187);
GAGGAAGAGG (SEQ ID NO:188);	AGGAAGAGGT (SEQ ID NO:189);
GGAAGAGGTG (SEQ ID NO:190);	GAAGAGGTGG (SEQ ID NO:191);
AAGAGGTGGG (SEQ ID NO:192);	AGAGGTGGGT (SEQ ID NO:193);
GAGGTGGGTT (SEQ ID NO:194);	AGGTGGGTTT (SEQ ID NO:195);
GGTGGGTTTT (SEQ ID NO:196);	GTGGGTTTTTC (SEQ ID NO:197);
TGGGTTTTTCC (SEQ ID NO:198);	GGGTTTTTCCA (SEQ ID NO:199);
GGTTTTTCCAG (SEQ ID NO:200);	GTTTTTCCAGT (SEQ ID NO:201);
TTTTCCAGTC (SEQ ID NO:202);	TTTCCAGTCA (SEQ ID NO:203);
TTCCAGTCAC (SEQ ID NO:204);	TCCAGTCACA (SEQ ID NO:205);
CCAGTCACAC (SEQ ID NO:206);	CAGTCACACC (SEQ ID NO:207);
AGTCACACCT (SEQ ID NO:208);	GTCACACCTC (SEQ ID NO:209);
TCACACCTCA (SEQ ID NO:210);	CACACCTCAG (SEQ ID NO:211);
ACACCTCAGG (SEQ ID NO:212);	CAGCTCAGGT (SEQ ID NO:213);
ACCTCAGGTA (SEQ ID NO:214);	CCTCAGGTAC (SEQ ID NO:215);
CTCAGGTACC (SEQ ID NO:216);	TCAGGTACCT (SEQ ID NO:217);
CAGGTACCTT (SEQ ID NO:218);	AGGTACCTTT (SEQ ID NO:219);
GGTACCTTTA (SEQ ID NO:220);	GTACCTTTAA (SEQ ID NO:221);
TACCTTTAAG (SEQ ID NO:222);	ACCTTTAAGA (SEQ ID NO:223);
CCTTTAAGAC (SEQ ID NO:224);	CTTTAAGACC (SEQ ID NO:225);
TTTAAGACCA (SEQ ID NO:226);	TTAAGACCAA (SEQ ID NO:227);
TAAGACCAAT (SEQ ID NO:228);	AAGACCAATG (SEQ ID NO:229);
AGACCAATGA (SEQ ID NO:230);	GACCAATGAC (SEQ ID NO:231);
ACCAATGACT (SEQ ID NO:232);	CCAATGACTT (SEQ ID NO:233);
CAATGACTTA (SEQ ID NO:234);	AATGACTTAC (SEQ ID NO:235);
ATGACTTACA (SEQ ID NO:236);	TGACTTACAA (SEQ ID NO:237);
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CTTACAAGGC (SEQ ID NO:240);	TTACAAGGCA (SEQ ID NO:241);
TACAAGGCAG (SEQ ID NO:242);	ACAAGGCAGC (SEQ ID NO:243);
CAAGGCAGCT (SEQ ID NO:244);	AAGGCAGCTG (SEQ ID NO:245);
AGGCAGCTGT (SEQ ID NO:246);	GGCAGCTGTA (SEQ ID NO:247);
GCAGCTGTAG (SEQ ID NO:248);	CAGCTGTAGA (SEQ ID NO:249);

- 233 -

AGCTGTAGAT (SEQ ID NO:250);	GCTGTAGATC (SEQ ID NO:251);
CTGTAGATCT (SEQ ID NO:252);	TGTAGATCTT (SEQ ID NO:253);
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ATCTTAGCCA (SEQ ID NO:258);	TCTTAGCCAC (SEQ ID NO:259);
CTTAGCCACT (SEQ ID NO:260);	TTAGCCACTT (SEQ ID NO:261);
TAGCCACTTT (SEQ ID NO:262);	AGCCACTTTT (SEQ ID NO:263);
GCCACTTTTT (SEQ ID NO:264);	CCACTTTTTA (SEQ ID NO:265);
CACTTTTTTAA (SEQ ID NO:266);	ACTTTTTTAAA (SEQ ID NO:267);
CTTTTTTAAAA (SEQ ID NO:268);	TTTTTAAAAG (SEQ ID NO:269);
TTTTTAAAAGA (SEQ ID NO:270);	TTTAAAAGAA (SEQ ID NO:271);
TTAAAAGAAA (SEQ ID NO:272);	TAAAAGAAAA (SEQ ID NO:273);
AAAAGAAAAG (SEQ ID NO:274);	AAAGAAAAGG (SEQ ID NO:275);
AAGAAAAGGG (SEQ ID NO:276);	AGAAAAGGGG (SEQ ID NO:277);
GAAAAGGGGG (SEQ ID NO:278);	AAAAGGGGGG (SEQ ID NO:279);
AAAGGGGGGA (SEQ ID NO:280);	AAGGGGGGAC (SEQ ID NO:281);
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GGGACTGGAA (SEQ ID NO:286);	GGACTGGAAG (SEQ ID NO:287);
GACTGGAAGG (SEQ ID NO:288);	ACTGGAAGGG (SEQ ID NO:289);
CTGGAAGGGC (SEQ ID NO:290);	TGGAAGGGCT (SEQ ID NO:291);
GGAAGGGCTA (SEQ ID NO:292);	GAAGGGCTAA (SEQ ID NO:293);
AAGGGCTAAT (SEQ ID NO:294);	AGGGCTAATT (SEQ ID NO:295);
GGGCTAATTC (SEQ ID NO:296);	GGCTAATTCA (SEQ ID NO:297);
GCTAATTCAC (SEQ ID NO:298);	CTAATTCACT (SEQ ID NO:299);
TAATTCACTC (SEQ ID NO:300);	AATTCACTCC (SEQ ID NO:301);
ATTCACTCCC (SEQ ID NO:302);	TTCACTCCCA (SEQ ID NO:303);
TCACTCCCAA (SEQ ID NO:304);	CACTCCCAAA (SEQ ID NO:305);
ACTCCCAAAG (SEQ ID NO:306);	CTCCCAAAGA (SEQ ID NO:307);
TCCCAAAGAA (SEQ ID NO:308);	CCCAAAGAAG (SEQ ID NO:309);
CCAAAGAAGA (SEQ ID NO:310);	CAAAGAAGAC (SEQ ID NO:311);
AAAGAAGACA (SEQ ID NO:312);	AAGAAGACAA (SEQ ID NO:313);
AGAAGACAAG (SEQ ID NO:314);	GAAGACAAGA (SEQ ID NO:315);
AAGACAAGAT (SEQ ID NO:316);	AGACAAGATA (SEQ ID NO:317);
GACAAGATAT (SEQ ID NO:318);	ACAAGATATC (SEQ ID NO:319);
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AGATATCCTT (SEQ ID NO:322);	GATATCCTTG (SEQ ID NO:323);
ATATCCTTGA (SEQ ID NO:324);	TATCCTTGAT (SEQ ID NO:325);

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- 234 -

ATCCTTGATC (SEQ ID NO:326); TCCTTGATCT (SEQ ID NO:327);
CCTTGATCTG (SEQ ID NO:328); CTTGATCTGT (SEQ ID NO:329);
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GATCTGTGGA (SEQ ID NO:332); ATCTGTGGAT (SEQ ID NO:333);
TCTGTGGATC (SEQ ID NO:334); CTGTGGATCT (SEQ ID NO:335);
TGTGGATCTA (SEQ ID NO:336); GTGGATCTAC (SEQ ID NO:337);
TGGATCTACC (SEQ ID NO:338); GGATCTACCA (SEQ ID NO:339);
GATCTACCAC (SEQ ID NO:340); ATCTACCACA (SEQ ID NO:341);
TCTACCACAC (SEQ ID NO:342); CTACCACACA (SEQ ID NO:343);
TACCACACAC (SEQ ID NO:344); ACCACACACA (SEQ ID NO:345);
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ACACAAGGCT (SEQ ID NO:350); CACAAGGCTA (SEQ ID NO:351);
ACAAGGCTAC (SEQ ID NO:352); CAAGGCTACT (SEQ ID NO:353);
AAGGCTACTT (SEQ ID NO:354); AGGCTACTTC (SEQ ID NO:355);
GGCTACTTCC (SEQ ID NO:356); GCTACTTCCC (SEQ ID NO:357);
CTACTTCCCT (SEQ ID NO:358); TACTTCCCTG (SEQ ID NO:359);
ACTTCCCTGA (SEQ ID NO:360); CTTCCCTGAT (SEQ ID NO:361);
TTCCCTGATT (SEQ ID NO:362); TCCCTGATTG (SEQ ID NO:363);
CCCTGATTGG (SEQ ID NO:364); CCTGATTGGC (SEQ ID NO:365);
CTGATTGGCA (SEQ ID NO:366); TGATTGGCAG (SEQ ID NO:367);
GATTGGCAGA (SEQ ID NO:368); ATTGGCAGAA (SEQ ID NO:369);
TTGGCAGAAC (SEQ ID NO:370); TGGCAGAACT (SEQ ID NO:371);
GGCAGAACTA (SEQ ID NO:372); GCAGAACTAC (SEQ ID NO:373);
CAGAACTACA (SEQ ID NO:374); AGAACTACAC (SEQ ID NO:375);
GAACTACACA (SEQ ID NO:376); AACTACACAC (SEQ ID NO:377);
ACTACACACC (SEQ ID NO:378); CTACACACCA (SEQ ID NO:379);
TACACACCAG (SEQ ID NO:380); ACACACCAGG (SEQ ID NO:381);
CACACCAGGG (SEQ ID NO:382); ACACCAGGGC (SEQ ID NO:383);
CACCAGGGCC (SEQ ID NO:384); ACCAGGGCCA (SEQ ID NO:385);
CCAGGGCCAG (SEQ ID NO:386); CAGGGCCAGG (SEQ ID NO:387);
AGGGCCAGGG (SEQ ID NO:388); GGGCCAGGGG (SEQ ID NO:389);
GGCCAGGGGT (SEQ ID NO:390); GCCAGGGGTC (SEQ ID NO:391);
CCAGGGGTCA (SEQ ID NO:392); CAGGGGTCAG (SEQ ID NO:393);
AGGGGTCAGA (SEQ ID NO:394); GGGGTCAGAT (SEQ ID NO:395);
GGGTCAGATA (SEQ ID NO:396); GGTCAGATAT (SEQ ID NO:397);
GTCAGATATC (SEQ ID NO:398); TCAGATATCC (SEQ ID NO:399);
CAGATATCCA (SEQ ID NO:400); AGATATCCAC (SEQ ID NO:401);

09146783-000309

- 235 -

GATATCCACT (SEQ ID NO:402);	ATATCCACTG (SEQ ID NO:403);
TATCCACTGA (SEQ ID NO:404);	ATCCACTGAC (SEQ ID NO:405);
TCCACTGACC (SEQ ID NO:406);	CCACTGACCT (SEQ ID NO:407);
CACTGACCTT (SEQ ID NO:408);	ACTGACCTTT (SEQ ID NO:409);
CTGACCTTTG (SEQ ID NO:410);	TGACCTTTGG (SEQ ID NO:411);
GACCTTTGGA (SEQ ID NO:412);	ACCTTTGGAT (SEQ ID NO:413);
CCTTTGGATG (SEQ ID NO:414);	CTTTGGATGG (SEQ ID NO:415);
TTTGGATGGT (SEQ ID NO:416);	TTGGATGGTG (SEQ ID NO:417);
TGGATGGTGC (SEQ ID NO:418);	GGATGGTGCT (SEQ ID NO:419);
GATGGTGCTA (SEQ ID NO:420);	ATGGTGCTAC (SEQ ID NO:421);
TGGTGCTACA (SEQ ID NO:422);	GGTGCTACAA (SEQ ID NO:423);
GTGCTACAAG (SEQ ID NO:424);	TGCTACAAGC (SEQ ID NO:425);
GCTACAAGCT (SEQ ID NO:426);	CTACAAGCTA (SEQ ID NO:427);
TACAAGCTAG (SEQ ID NO:428);	ACAAGCTAGT (SEQ ID NO:429);
CAAGCTAGTA (SEQ ID NO:430);	AAGCTAGTAC (SEQ ID NO:431);
AGCTAGTACC (SEQ ID NO:432);	GCTAGTACCA (SEQ ID NO:433);
CTAGTACCAG (SEQ ID NO:434);	TAGTACCAGT (SEQ ID NO:435);
AGTACCAGTT (SEQ ID NO:436);	GTACCAGTTG (SEQ ID NO:437);
TACCAGTTGA (SEQ ID NO:438);	ACCAGTTGAG (SEQ ID NO:439);
CCAGTTGAGC (SEQ ID NO:440);	CAGTTGAGCC (SEQ ID NO:441);
AGTTGAGCCA (SEQ ID NO:442);	GTTGAGCCAG (SEQ ID NO:443);
TTGAGCCAGA (SEQ ID NO:444);	TGAGCCAGAT (SEQ ID NO:445);
GAGCCAGATA (SEQ ID NO:446);	AGCCAGATAA (SEQ ID NO:447);
GCCAGATAAG (SEQ ID NO:448);	CCAGATAAGG (SEQ ID NO:449);
CAGATAAGGT (SEQ ID NO:450);	AGATAAGGTA (SEQ ID NO:451);
GATAAGGTAG (SEQ ID NO:452);	ATAAGGTAGA (SEQ ID NO:453);
TAAGGTAGAA (SEQ ID NO:454);	AAGGTAGAAG (SEQ ID NO:455);
AGGTAGAAGA (SEQ ID NO:456);	GGTAGAAGAG (SEQ ID NO:457);
GTAGAAGAGG (SEQ ID NO:458);	TAGAAGAGGC (SEQ ID NO:459);
AGAAGAGGCC (SEQ ID NO:460);	GAAGAGGCCA (SEQ ID NO:461);
AAGAGGCCAA (SEQ ID NO:462);	AGAGGCCAAT (SEQ ID NO:463);
GAGGCCAATA (SEQ ID NO:464);	AGGCCAATAA (SEQ ID NO:465);
GGCCAATAAA (SEQ ID NO:466);	GCCAATAAAG (SEQ ID NO:467);
CCAATAAAGG (SEQ ID NO:468);	CAATAAAGGA (SEQ ID NO:469);
AATAAAGGAG (SEQ ID NO:470);	ATAAAGGAGA (SEQ ID NO:471);
TAAAGGAGAG (SEQ ID NO:472);	AAAGGAGAGA (SEQ ID NO:473);
AAGGAGAGAA (SEQ ID NO:474);	AGGAGAGAAC (SEQ ID NO:475);
GGAGAGAACA (SEQ ID NO:476);	GAGAGAACAC (SEQ ID NO:477);

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- 236 -

AGAGAACACC (SEQ ID NO:478); GAGAACACCA (SEQ ID NO:479);
AGAACACCAG (SEQ ID NO:480); GAACACCAGC (SEQ ID NO:481);
AACACCAGCT (SEQ ID NO:482); ACACCAGCTT (SEQ ID NO:483);
CACCAGCTTG (SEQ ID NO:484); ACCAGCTTGT (SEQ ID NO:485);
CCAGCTTGTT (SEQ ID NO:486); CAGCTTGTTA (SEQ ID NO:487);
AGCTTGTTAC (SEQ ID NO:488); GCTTGTTACA (SEQ ID NO:489);
CTTGTTACAC (SEQ ID NO:490); TTGTTACACC (SEQ ID NO:491);
TGTTACACCC (SEQ ID NO:492); GTTACACCCT (SEQ ID NO:493);
TTACACCCTG (SEQ ID NO:494); TACACCCTGT (SEQ ID NO:495);
ACACCCTGTG (SEQ ID NO:496); CACCCTGTGA (SEQ ID NO:497);
ACCCTGTGAG (SEQ ID NO:498); CCCTGTGAGC (SEQ ID NO:499);
CCTGTGAGCC (SEQ ID NO:500); CTGTGAGCCT (SEQ ID NO:501);
TGTGAGCCTG (SEQ ID NO:502); GTGAGCCTGC (SEQ ID NO:503);
TGAGCCTGCA (SEQ ID NO:504); GAGCCTGCAT (SEQ ID NO:505);
AGCCTGCATG (SEQ ID NO:506); GCCTGCATGG (SEQ ID NO:507);
CCTGCATGGA (SEQ ID NO:508); CTGCATGGAA (SEQ ID NO:509);
TGCATGGAAT (SEQ ID NO:510); GCATGGAATG (SEQ ID NO:511);
CATGGAATGG (SEQ ID NO:512); ATGGAATGGA (SEQ ID NO:513);
TGGAATGGAT (SEQ ID NO:514); GGAATGGATG (SEQ ID NO:515);
GAATGGATGA (SEQ ID NO:516); AATGGATGAC (SEQ ID NO:517);
ATGGATGACC (SEQ ID NO:518); TGGATGACCC (SEQ ID NO:519);
GGATGACCCT (SEQ ID NO:520); GATGACCCTG (SEQ ID NO:521);
ATGACCCTGA (SEQ ID NO:522); TGACCCTGAG (SEQ ID NO:523);
GACCCTGAGA (SEQ ID NO:524); ACCCTGAGAG (SEQ ID NO:525);
CCCTGAGAGA (SEQ ID NO:526); CCTGAGAGAG (SEQ ID NO:527);
CTGAGAGAGA (SEQ ID NO:528); TGAGAGAGAA (SEQ ID NO:529);
GAGAGAGAAG (SEQ ID NO:530); AGAGAGAAGT (SEQ ID NO:531);
GAGAGAAGTG (SEQ ID NO:532); AGAGAAGTGT (SEQ ID NO:533);
GAGAAGTGTT (SEQ ID NO:534); AGAAGTGTTA (SEQ ID NO:535);
GAAGTGTTAG (SEQ ID NO:536); AAGTGTTAGA (SEQ ID NO:537);
AGTGTTAGAG (SEQ ID NO:538); GTGTTAGAGT (SEQ ID NO:539);
TGTTAGAGTG (SEQ ID NO:540); GTTAGAGTGG (SEQ ID NO:541);
TTAGAGTGGA (SEQ ID NO:542); TAGAGTGGAG (SEQ ID NO:543);
AGAGTGGAGG (SEQ ID NO:544); GAGTGGAGGT (SEQ ID NO:545);
AGTGGAGGTT (SEQ ID NO:546); GTGGAGGTTT (SEQ ID NO:547);
TGGAGGTTTG (SEQ ID NO:548); GGAGGTTTGA (SEQ ID NO:549);
GAGGTTTGAC (SEQ ID NO:550); AGGTTTGACA (SEQ ID NO:551);
GGTTTGACAG (SEQ ID NO:552); GTTTGACAGC (SEQ ID NO:553);

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950606.p:\open\gh.HIV1.USA\237

- 237 -

TTTGACAGCC (SEQ ID NO:554); TTGACAGCCG (SEQ ID NO:555);
 TGACAGCCGC (SEQ ID NO:556); GACAGCCGCC (SEQ ID NO:557);
 ACAGCCGCCT (SEQ ID NO:558); CAGCCGCCTA (SEQ ID NO:559);
 AGCCGCCTAG (SEQ ID NO:560); GCCGCCTAGC (SEQ ID NO:561);
 CCGCCTAGCA (SEQ ID NO:562); CGCCTAGCAT (SEQ ID NO:563);
 GCCTAGCATT (SEQ ID NO:564); CCTAGCATT (SEQ ID NO:565);
 CTAGCATTTTC (SEQ ID NO:566); TAGCATTTTCA (SEQ ID NO:567);
 AGCATTTTCAT (SEQ ID NO:568); GCATTTTCATC (SEQ ID NO:569);
 CATTTTCATCA (SEQ ID NO:570); ATTTTCATCAC (SEQ ID NO:571);
 TTTTCATCACG (SEQ ID NO:572); TTCATCACGT (SEQ ID NO:573);
 TCATCACGTG (SEQ ID NO:574); CATCACGTGG (SEQ ID NO:575);
 ATCACGTGGC (SEQ ID NO:576); TCACGTGGCC (SEQ ID NO:577);
 CACGTGGCCC (SEQ ID NO:578); ACGTGGCCCG (SEQ ID NO:579);
 CGTGGCCCGA (SEQ ID NO:580); GTGGCCCGAG (SEQ ID NO:581);
 TGGCCCGAGA (SEQ ID NO:582); GGCCCGAGAG (SEQ ID NO:583);
 GCCCGAGAGC (SEQ ID NO:584); CCCGAGAGCT (SEQ ID NO:585);
 CCGAGAGCTG (SEQ ID NO:586); CGAGAGCTGC (SEQ ID NO:587);
 GAGAGCTGCA (SEQ ID NO:588); AGAGCTGCAT (SEQ ID NO:589);
 GAGCTGCATC (SEQ ID NO:590); AGCTGCATCC (SEQ ID NO:591);
 GCTGCATCCG (SEQ ID NO:592); CTGCATCCGG (SEQ ID NO:593);
 TGCATCCGGA (SEQ ID NO:594); GCATCCGGAG (SEQ ID NO:595);
 CATCCGGAGT (SEQ ID NO:596); ATCCGGAGTA (SEQ ID NO:597);
 TCCGGAGTAC (SEQ ID NO:598); CCGGAGTACT (SEQ ID NO:599);
 CGGAGTACTT (SEQ ID NO:600); GGAGTACTTC (SEQ ID NO:601);
 GAGTACTTCA (SEQ ID NO:602); AGTACTTCAA (SEQ ID NO:603);
 GTACTTCAAG (SEQ ID NO:604); TACTTCAAGA (SEQ ID NO:605);
 ACTTCAAGAA (SEQ ID NO:606); CTTCAAGAAC (SEQ ID NO:607);
 TTCAAGAACT (SEQ ID NO:608); TCAAGAACTG (SEQ ID NO:609);
 CAAGAACTGC (SEQ ID NO:610); AAGAACTGCT (SEQ ID NO:611);
 AGAACTGCTG (SEQ ID NO:612); GAACTGCTGA (SEQ ID NO:613).

44. A method according to claim 38 wherein said deletion encompasses at least one of the following decanucleotide deletions from the *nef* gene:

ACCAGCTTGT [SEQ ID NO:803]	CCAGCTTGTT [SEQ ID NO:804]
CAGCTTGTTA [SEQ ID NO:805]	AGCTTGTTAC [SEQ ID NO:806]
GCTTGTTACA [SEQ ID NO:807]	CTTGTTACAC [SEQ ID NO:808]
TTGTTACACC [SEQ ID NO:809]	TGTTACACCC [SEQ ID NO:810]

504463-000000

950606, p1, opar1, HIV1, USA, 238

- 238 -

GTTACACCCT [SEQ ID NO:811]	TTACACCCTG [SEQ ID NO:812]
TACACCCTGT [SEQ ID NO:813]	ACACCCTGTG [SEQ ID NO:814]
CACCCTGTGA [SEQ ID NO:815]	ACCCTGTGAG [SEQ ID NO:816]
CCCTGTGAGC [SEQ ID NO:817]	CCTGTGAGCC [SEQ ID NO:818]
CTGTGAGCCT [SEQ ID NO:819]	TGTGAGCCTG [SEQ ID NO:820]
GTGAGCCTGC [SEQ ID NO:821]	TGAGCCTGCA [SEQ ID NO:822]
GAGCCTGCAT [SEQ ID NO:823]	AGCCTGCATG [SEQ ID NO:824]
GCCTGCATGG [SEQ ID NO:825]	CCTGCATGGA [SEQ ID NO:826]
CTGCATGGAA [SEQ ID NO:827]	TGCATGGAAT [SEQ ID NO:828]
GCATGGAATG [SEQ ID NO:829]	CATGGAATGG [SEQ ID NO:830]
ATGGAATGGA [SEQ ID NO:831]	TGGAATGGAT [SEQ ID NO:832]
GGAATGGATG [SEQ ID NO:833]	GAATGGATGA [SEQ ID NO:834]
AATGGATGAC [SEQ ID NO:835]	ATGGATGACC [SEQ ID NO:836]
TGGATGACCC [SEQ ID NO:837]	GGATGACCCT [SEQ ID NO:838]
GATGACCCTG [SEQ ID NO:839]	ATGACCCTGA [SEQ ID NO:840]
TGACCCTGAG [SEQ ID NO:841]	

45. A method according to claim 38 wherein said deletion encompasses at least one of the following decanucleotides from the LTR region of HIV-1_{NL43}:

GCTTTTGGCC (SEQ ID NO:652);	CTTTTGCCT (SEQ ID NO:653);
TTTTTGCCTG (SEQ ID NO:654);	TTTTCCTGT (SEQ ID NO:655);
TTTGCCTGTA (SEQ ID NO:656);	TTGCCTGTAC (SEQ ID NO:657);
TGCCTGTACT (SEQ ID NO:658);	GCCTGTACTG (SEQ ID NO:659);
CCTGTACTGG (SEQ ID NO:660);	CTGTACTGGG (SEQ ID NO:661);
TGTACTGGGT (SEQ ID NO:662);	GTA CTGGGTC (SEQ ID NO:663);
TACTGGGTCT (SEQ ID NO:664);	ACTGGGTCTC (SEQ ID NO:665);
CTGGGTCTCT (SEQ ID NO:666);	TGGGTCTCTC (SEQ ID NO:667);
GGGTCTCTCT (SEQ ID NO:668);	GGTCTCTCTG (SEQ ID NO:669);
GTCTCTCTGG (SEQ ID NO:670);	TCTCTCTGGT (SEQ ID NO:671);
CTCTCTGGTT (SEQ ID NO:672);	TCTCTGGTTA (SEQ ID NO:673);
CTCTGGTTAG (SEQ ID NO:674);	TCTCTGGTTA (SEQ ID NO:675);
CTGGTTAGAC (SEQ ID NO:676);	TGGTTAGACC (SEQ ID NO:677);
GGTTAGACCA (SEQ ID NO:678);	GTTAGACCAG (SEQ ID NO:679);
TTAGACCAGA (SEQ ID NO:680);	TAGACCAGAT (SEQ ID NO:681);
AGACCAGATC (SEQ ID NO:682);	GACCAGATCT (SEQ ID NO:683);
ACCAGATCTG (SEQ ID NO:684);	CCAGATCTGA (SEQ ID NO:685);
CAGATCTGAG (SEQ ID NO:686);	AGATCTGAGC (SEQ ID NO:687);

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Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in the YEA medium for 24 h at 28°C. The cell concentration of the strains was adjusted to 10⁸ cells/ml. The cell suspension was mixed with the plant tissue and the transformation efficiency was determined. The results were expressed as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (*P* < 0.05) between the strains.

GATCTGAGCC	(SEQ ID NO:688);	ATCTGAGCCT	(SEQ ID NO:689);
TCTGAGCCTG	(SEQ ID NO:690);	CTGAGCCTGG	(SEQ ID NO:691);
TGAGCCTGGG	(SEQ ID NO:692);	GAGCCTGGGA	(SEQ ID NO:693);
AGCCTGGGAG	(SEQ ID NO:694);	GCCTGGGAGC	(SEQ ID NO:695);
CCTGGGAGCT	(SEQ ID NO:696);	CTGGGAGCTC	(SEQ ID NO:697);
TGGGAGCTCT	(SEQ ID NO:698);	GGGAGCTCTC	(SEQ ID NO:699);
GGAGCTCTCT	(SEQ ID NO:700);	GAGCTCTCTG	(SEQ ID NO:701);
AGCTCTCTGG	(SEQ ID NO:702);	GCTCTCTGGC	(SEQ ID NO:703);
CTCTCTGGCT	(SEQ ID NO:704);	TCTCTGGCTA	(SEQ ID NO:705);
CTCTGGCTAA	(SEQ ID NO:706);	TCTGGCTAAC	(SEQ ID NO:707);
CTGGCTAACT	(SEQ ID NO:708);	TGGCTAACTA	(SEQ ID NO:709);
GGCTAACTAG	(SEQ ID NO:710);	GCTAACTAGG	(SEQ ID NO:711);
CTAACTAGGG	(SEQ ID NO:712);	TAACTAGGGA	(SEQ ID NO:713);
AACTAGGGAA	(SEQ ID NO:714);	ACTAGGGAAC	(SEQ ID NO:715);
CTAGGGGAACC	(SEQ ID NO:716);	TAGGGGAACCC	(SEQ ID NO:717);
AGGGAACCCA	(SEQ ID NO:718);	GGGAACCCAC	(SEQ ID NO:719);
GGAACCCACT	(SEQ ID NO:720);	GAACCCACTG	(SEQ ID NO:721);
AACCCACTGC	(SEQ ID NO:722);	ACCCACTGCT	(SEQ ID NO:723);
CCCACTGCTT	(SEQ ID NO:724);	CCACTGCTTA	(SEQ ID NO:725);
CACTGCTTAA	(SEQ ID NO:726);	ACTGCTTAAG	(SEQ ID NO:727);
CTGCTTAAGC	(SEQ ID NO:728);	TGCTTAAGCC	(SEQ ID NO:729);
GCTTAAGCCT	(SEQ ID NO:730);	CTTAAGCCTC	(SEQ ID NO:731);
TTAAGCCTCA	(SEQ ID NO:732);	TAAGCCTCAA	(SEQ ID NO:733);
AAGCCTCAAT	(SEQ ID NO:734);	AGCCTCAATA	(SEQ ID NO:735);
GCCTCAATAA	(SEQ ID NO:736);	CCTCAATAAA	(SEQ ID NO:737);
CTCAATAAAG	(SEQ ID NO:738);	TCAATAAAGC	(SEQ ID NO:739);
CAATAAAGCT	(SEQ ID NO:740);	AATAAAGCTT	(SEQ ID NO:741);
ATAAAGCTTG	(SEQ ID NO:742);	TAAAGCTTGC	(SEQ ID NO:743);
AAAGCTTGCC	(SEQ ID NO:744);	AAGCTTGCCCT	(SEQ ID NO:745);
AGCTTGCCCT	(SEQ ID NO:746);	GCTTGCCCTG	(SEQ ID NO:747);
CTTGCCCTTGA	(SEQ ID NO:748);	TTGCCCTTGAG	(SEQ ID NO:749);
TGCCCTTGAGT	(SEQ ID NO:750);	GCCTTGAGTG	(SEQ ID NO:751);
CCTTGAGTGC	(SEQ ID NO:752);	CTTGAGTGCT	(SEQ ID NO:753);
TTGAGTGCTT	(SEQ ID NO:754);	TGAGTGCTTC	(SEQ ID NO:755);
GAGTGCTTCA	(SEQ ID NO:756);	AGTGCTTCAA	(SEQ ID NO:757);
GTGCTTCAAG	(SEQ ID NO:758);	TGCTTCAAGT	(SEQ ID NO:759);
GCTTCAAGTA	(SEQ ID NO:760);	CTTCAAGTAG	(SEQ ID NO:761);
TTCAAGTAGT	(SEQ ID NO:762);	TCAAGTAGTG	(SEQ ID NO:763);

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- 240 -

CAAGTAGTGT (SEQ ID NO:764); AAGTAGTGTG (SEQ ID NO:765);
 AGTAGTGTGT (SEQ ID NO:766); GTAGTGTGTG (SEQ ID NO:767);
 TAGTGTGTGC (SEQ ID NO:768); AGTGTGTGCC (SEQ ID NO:769);
 GTGTGTGCCC (SEQ ID NO:770); TGTGTGCCCC (SEQ ID NO:771);
 GTGTGCCCCG (SEQ ID NO:772); TGTGCCCCGTC (SEQ ID NO:773);
 GTGCCCCGTCT (SEQ ID NO:774); TGCCCCGTCTG (SEQ ID NO:775);
 GCCCGTCTGT (SEQ ID NO:776); CCCGTCTGTT (SEQ ID NO:777);
 CCGTCTGTTG (SEQ ID NO:778); CGTCTGTTGT (SEQ ID NO:779);
 GTCTGTTGTG (SEQ ID NO:780); TCTGTTGTGT (SEQ ID NO:781);
 CTGTTGTGTG (SEQ ID NO:782); TGTGTGTGA (SEQ ID NO:783);
 GTTGTGTGAC (SEQ ID NO:784); TTGTGTGACT (SEQ ID NO:785);
 TGTGTGACTC (SEQ ID NO:786); GTGTGACTCT (SEQ ID NO:787);
 TGTGTGACTC (SEQ ID NO:788); GTGTGACTCT (SEQ ID NO:789);
 TGTGACTCTG (SEQ ID NO:790); GTGACTCTGG (SEQ ID NO:791);
 TGACTCTGGT (SEQ ID NO:792); GACTCTGGTA (SEQ ID NO:793);
 ACTCTGGTAA (SEQ ID NO:794); CTCTGGTAAC (SEQ ID NO:795);
 TCTGGTAACT (SEQ ID NO:796); CTGGTAACTA (SEQ ID NO:797);
 TGGTAACTAG (SEQ ID NO:798); GGTAAC TAGA (SEQ ID NO:799).

46. A method according to claim 30 wherein said HIV-1 isolate has the identifying characteristics of HIV-1 isolate ECACC Accession No. V94101706 or HIV-1 isolate ECACC Accession No. V941031169 or HIV-1 isolate ECACC Accession No. V95031022.

47. A method according to claim 30 wherein the HIV-1 isolate is reactive to antibodies to a glycoprotein of HIV-1, is capable of inducing an immune response of *gag*, *pol* and/or *env* and which is incapable of directing synthesis of a *nef* gene product or a full length *nef* gene product.

48. A method according to claim 47 wherein the glycoprotein is at least one of gp41-45, gp120 and/or gp160.

49. A method for vaccinating an individual against the development of AIDS or AIDS related diseases, said method comprising administering to said individual a non-pathogenic isolate of HIV-1 in an amount effective to infect target cells and to generate

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- 241 -

target cells carrying DNA derived from said non-pathogenic HIV-1.

50. A method according to claim 49 wherein said isolate is capable of stimulating an immune response in a human or primate against at least one glycoprotein on HIV-1 whilst not substantially reducing proliferative responses and cytokine production to a mitogen in said human or primate compared to a healthy, non-infected human or primate subject.

51. A method according to claim 50 wherein said isolate carries one or more mutations in its genome resulting in the inability to direct synthesis of at least one polypeptide or protein from a pathogenic strain of HIV-1.

52. A method according to claim 49 wherein said isolate carries one or more mutations in its genome resulting in said genome directing synthesis of a truncated form of a polypeptide or protein from a pathogenic strain of HIV-1.

53. A method according to claim 51 or 52 wherein said HIV-1 isolate carries a mutation in its *nef* gene and/or long terminal repeat (LTR) region or in a functionally equivalent location in the HIV-1 genome.

54. A method according to claim 53 wherein said HIV-1 isolate is reactive to antibodies to gp41-45, gp120 and/or gp160 of HIV-1 and carries a deletion of at least ten contiguous nucleotides in a region corresponding to the *nef* gene and/or LTR region of pathogenic HIV-1.

55. A method according to claim 53 wherein said HIV-1 isolate encodes a modified Nef protein without amino acids 162 to 177 of wild-type HIV-1_{NL43} Nef.

56. A method according to claim 54 or 55 wherein said HIV-1 isolate is capable of inducing an immune response to at least one of *gag*, *pol* and/or *env*.

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- 242 -

57. A method according to claim 56 wherein said HIV-1 isolate carries a deletion in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43}.

58. A method according to claim 57 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(i)	8830-8862;
	(ii)	9009-9035;
	(iii)	9019-9029; and
	(iv)	9033-9049.

59. A method according to claim 57 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(v)	9281-9371;
	(vi)	9281-9362;
	(vii)	9105-9224; and
	(viii)	9271-9370.

60. A method according to claim 57 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(ix)	8882-8928;
	(x)	8850-9006;
	(xi)	8792-9041; and
	(xii)	9112-9204.

61. A method according to claim 57 wherein said isolate carries a deletion in its genome of at least 10 nucleotides within a region selected from the list consisting of:

nucleotide	(xiii)	9105-9224;
	(xiv)	9389-9395; and
	(xv)	9281-9366.

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- 243 -

62. A method according to claim 57 wherein said deletion encompasses at least one of the following decanucleotides from the nef gene of HIV-1_{ML43}:

ATGGGTGGCA (SEQ ID NO:2);	TGGGTGGCAA (SEQ ID NO:3);
GGGTGGCAAG (SEQ ID NO:4);	GGTGGCAAGT (SEQ ID NO:5);
GTGGCAAGTG (SEQ ID NO:6);	TGGCAAGTGG (SEQ ID NO:7);
GGCAAGTGGT (SEQ ID NO:8);	GCAAGTGGTC (SEQ ID NO:9);
CAAGTGGTCA (SEQ ID NO:10);	AAAGTGGTCAA (SEQ ID NO:11);
AGTGGTCAAA (SEQ ID NO:12);	GTGGTCAAAA (SEQ ID NO:13);
TGGTCAAAA (SEQ ID NO:14);	GGTCAAAAAG (SEQ ID NO:15);
GTCAAAAAGT (SEQ ID NO:16);	TCAAAAAGTA (SEQ ID NO:17);
CAAAAAGTAG (SEQ ID NO:18);	AAAAGTAGT (SEQ ID NO:19);
AAAAGTAGTG (SEQ ID NO:20);	AAAGTAGTGT (SEQ ID NO:21);
AAGTAGTGTG (SEQ ID NO:22);	AGTAGTGTGA (SEQ ID NO:23);
GTAGTGTGAT (SEQ ID NO:24);	TAGTGTGATT (SEQ ID NO:25);
AGTGTGATTG (SEQ ID NO:26);	GTGTGATTGG (SEQ ID NO:27);
TGTGATTGGA (SEQ ID NO:28);	GTGATTGGAT (SEQ ID NO:29);
TGATTGGATG (SEQ ID NO:30);	GATTGGATGG (SEQ ID NO:31);
ATTGGATGGC (SEQ ID NO:32);	TGGATGGCC (SEQ ID NO:33);
TGGATGGCCT (SEQ ID NO:34);	GGATGGCCTG (SEQ ID NO:35);
GATGGCCTGC (SEQ ID NO:36);	ATGGCCTGCT (SEQ ID NO:37);
TGGCCTGCTG (SEQ ID NO:38);	GGGCTGCTGT (SEQ ID NO:39);
GCCTGCTGTA (SEQ ID NO:40);	CCTGCTGTAA (SEQ ID NO:41);
CTGCTGTAAG (SEQ ID NO:42);	TGCTGTAAGG (SEQ ID NO:43);
GCTGTAAGGG (SEQ ID NO:44);	CTGTAAGGGA (SEQ ID NO:45);
TGTAAGGGAA (SEQ ID NO:46);	GTAAGGGAAA (SEQ ID NO:47);
TAAGGGAAAG (SEQ ID NO:48);	AAGGGAAAGA (SEQ ID NO:49);
AGGGAAAGAA (SEQ ID NO:50);	GGGAAAGAAT (SEQ ID NO:51);
GGAAAGAATG (SEQ ID NO:52);	GAAAGAATGA (SEQ ID NO:53);
AAAGAATGAG (SEQ ID NO:54);	AAGAATGAGA (SEQ ID NO:55);
AGAATGAGAC (SEQ ID NO:56);	GAGTGAAGAC (SEQ ID NO:57);
AATGAGACGA (SEQ ID NO:58);	ATGAGACGAG (SEQ ID NO:59);
TGAGACGAGC (SEQ ID NO:60);	GAGACGAGCT (SEQ ID NO:61);
AGACGAGCTG (SEQ ID NO:62);	GACGAGCTGA (SEQ ID NO:63);
ACGAGCTGAG (SEQ ID NO:64);	CGAGCTGAGC (SEQ ID NO:65);
GAGCTGAGCC (SEQ ID NO:66);	AGCTGAGCCA (SEQ ID NO:67);
GCTGAGCCAG (SEQ ID NO:68);	CTGAGCCAGC (SEQ ID NO:69);
TGAGCCAGCA (SEQ ID NO:70);	GAGCCAGCAG (SEQ ID NO:71);

09146793-090393

AGCCAGCAGC (SEQ ID NO:72);	GCCAGCAGCA (SEQ ID NO:73);
CCAGCAGCAG (SEQ ID NO:74);	CAGCAGCAGA (SEQ ID NO:75);
AGCAGCAGAT (SEQ ID NO:76);	GCAGCAGATG (SEQ ID NO:77);
CAGCAGATGG (SEQ ID NO:78);	AGCAGATGGG (SEQ ID NO:79);
GCAGATGGGG (SEQ ID NO:80);	CAGATGGGGT (SEQ ID NO:81);
AGATGGGGTG (SEQ ID NO:82);	GATGGGGTGG (SEQ ID NO:83);
ATGGGGTGGG (SEQ ID NO:84);	TGGGGTGGGA (SEQ ID NO:85);
GGGGTGGGAG (SEQ ID NO:86);	GGGTGGGGAG (SEQ ID NO:87);
GGTGGGAGCA (SEQ ID NO:88);	GTGGGAGCGA (SEQ ID NO:89);
TGGGAGCACT (SEQ ID NO:90);	GGGAGCACTA (SEQ ID NO:91);
GGAGCACTAT (SEQ ID NO:92);	GAGCACTATC (SEQ ID NO:93);
AGCACTATCT (SEQ ID NO:94);	GCACTATCTC (SEQ ID NO:95);
CAGTATCTCG (SEQ ID NO:96);	AGTATCTCGA (SEQ ID NO:97);
GTATCTCGAG (SEQ ID NO:98);	TATCTCGAGA (SEQ ID NO:99);
ATCTCGAGAC (SEQ ID NO:100);	TCTCGAGAGC (SEQ ID NO:101);
CTCGAGACCT (SEQ ID NO:102);	TCGAGACCTA (SEQ ID NO:103);
CGAGACCTAG (SEQ ID NO:104);	GAGACCTAGA (SEQ ID NO:105);
AGACCTAGAA (SEQ ID NO:106);	GACCTAGAAA (SEQ ID NO:107);
ACCTAGAAAA (SEQ ID NO:108);	OCTAGAAAAA (SEQ ID NO:109);
CTAGAAAAAC (SEQ ID NO:110);	TAGAAAAACA (SEQ ID NO:111);
AGAAAAACAT (SEQ ID NO:112);	GAAAAACATG (SEQ ID NO:113);
AAAAACATGG (SEQ ID NO:114);	AAAACATGGA (SEQ ID NO:115);
AAACATGGAG (SEQ ID NO:116);	AACATGGAGC (SEQ ID NO:117);
ACATGGAGCA (SEQ ID NO:118);	CATGGAGCAA (SEQ ID NO:119);
ATGGAGCAAT (SEQ ID NO:120);	TGGAGCAATC (SEQ ID NO:121);
GGAGCAATCA (SEQ ID NO:122);	GAGCAATCAC (SEQ ID NO:123);
AGCAATCACA (SEQ ID NO:124);	GCAATCACAA (SEQ ID NO:125);
CAATCACAGG (SEQ ID NO:126);	AATCACAGGT (SEQ ID NO:127);
ATCACAGGTA (SEQ ID NO:128);	TCACAGGTAG (SEQ ID NO:129);
CACAGGTAGC (SEQ ID NO:130);	ACAAGGTAGCA (SEQ ID NO:131);
CAAGTAGCAA (SEQ ID NO:132);	AAGTAGCAAT (SEQ ID NO:133);
AGTAGCAATA (SEQ ID NO:134);	GTAGCAATAC (SEQ ID NO:135);
TAGCAATACA (SEQ ID NO:136);	AGCAATACAG (SEQ ID NO:137);
GCAATACAGC (SEQ ID NO:138);	CAATACAGCA (SEQ ID NO:139);
AATACAGCAG (SEQ ID NO:140);	ATACAGCAGC (SEQ ID NO:141);
TACAGCAGCT (SEQ ID NO:142);	ACAGCAGCTA (SEQ ID NO:143);
CAGCAGCTAA (SEQ ID NO:144);	AGCAGCTAAC (SEQ ID NO:145);
GCAGCTAACA (SEQ ID NO:146);	CAGCTAACAA (SEQ ID NO:147);

- 245 -

AGCTAACCAAT (SEQ ID NO:148);	GCTAACCAATG (SEQ ID NO:149);
CTAACCAATGC (SEQ ID NO:150);	TAACCAATGCT (SEQ ID NO:151);
AACAATGCTG (SEQ ID NO:152);	ACAATGCTGC (SEQ ID NO:153);
CAATGCTGCT (SEQ ID NO:154);	AATGCTGCTT (SEQ ID NO:155);
ATGCTGCTTG (SEQ ID NO:156);	TGCTGCTTGT (SEQ ID NO:157);
GCTGCTTGTG (SEQ ID NO:158);	CTGCTTGTGC (SEQ ID NO:159);
TGCTTGTGCC (SEQ ID NO:160);	GCTTGTGCCT (SEQ ID NO:161);
CTTGTGCCTG (SEQ ID NO:162);	TTGTGCCTGG (SEQ ID NO:163);
TGTGCCTGGC (SEQ ID NO:164);	GTGCCTGGCT (SEQ ID NO:165);
TGCCTGGCTA (SEQ ID NO:166);	GCCTGGCTAG (SEQ ID NO:167);
CCTGGCTAGA (SEQ ID NO:168);	CTGGCTAGAA (SEQ ID NO:169);
TGGCTAGAAG (SEQ ID NO:170);	GGCTAGAAAG (SEQ ID NO:171);
GCTAGAAACA (SEQ ID NO:172);	CTAGAAAGAC (SEQ ID NO:173);
TAGAAGCACA (SEQ ID NO:174);	AGAAGCACAA (SEQ ID NO:175);
GAAGCACAA (SEQ ID NO:176);	AAGCACAAAG (SEQ ID NO:177);
AGCACAAAG (SEQ ID NO:178);	GCACAAAGAG (SEQ ID NO:179);
CACAAAGAG (SEQ ID NO:180);	ACAAGAGAG (SEQ ID NO:181);
CAAGAGGAG (SEQ ID NO:182);	AAGAGGAGAG (SEQ ID NO:183);
AGAGGAGGAA (SEQ ID NO:184);	GAGGAGGAG (SEQ ID NO:185);
AGGAGGAGAA (SEQ ID NO:186);	GGAGGAGAG (SEQ ID NO:187);
GAGGAGAGAG (SEQ ID NO:188);	AGGAGAGAGT (SEQ ID NO:189);
GGAGAGAGTG (SEQ ID NO:190);	GAAGAGGTGG (SEQ ID NO:191);
AAGAGGTGGG (SEQ ID NO:192);	AGAGGTGGGT (SEQ ID NO:193);
GAGGTGGGTT (SEQ ID NO:194);	AGGTGGGTTT (SEQ ID NO:195);
GGTGGGTTTT (SEQ ID NO:196);	GTGGGTTTTT (SEQ ID NO:197);
TGGGTTTTTCC (SEQ ID NO:198);	GGTTTTTCCA (SEQ ID NO:199);
GGTTTTTCCAG (SEQ ID NO:200);	GTTTTTCCAGT (SEQ ID NO:201);
TTTTTCCAGTC (SEQ ID NO:202);	TTTCCAGTCA (SEQ ID NO:203);
TTCCAGTCAC (SEQ ID NO:204);	TCCAGTCACA (SEQ ID NO:205);
CCAGTCACAC (SEQ ID NO:206);	CAGTCACACC (SEQ ID NO:207);
AGTCACACCT (SEQ ID NO:208);	GTCACACCTC (SEQ ID NO:209);
TCACACCTCA (SEQ ID NO:210);	CACACCTCAG (SEQ ID NO:211);
ACACCTCAGG (SEQ ID NO:212);	CAGCTCAGGT (SEQ ID NO:213);
ACCTCAGGTA (SEQ ID NO:214);	CCTCAGGTAC (SEQ ID NO:215);
CTCAGGTACC (SEQ ID NO:216);	TCAGGTACCT (SEQ ID NO:217);
CAGGTACCTT (SEQ ID NO:218);	AGGTACCTTT (SEQ ID NO:219);
GGTACCTTTA (SEQ ID NO:220);	GTACCTTTAA (SEQ ID NO:221);
TACCTTTAAG (SEQ ID NO:222);	ACCTTTAAGA (SEQ ID NO:223);

938604,ptepapq,HBV1.037C46

- 246 -

CCTTTAAGAC (SEQ ID NO:224); CTTTAAGACC (SEQ ID NO:225);
TTTAAGACCA (SEQ ID NO:226); TTAAGACCAA (SEQ ID NO:227);
TAAGACCAAT (SEQ ID NO:228); AAGACCAATG (SEQ ID NO:229);
AGACCAATGA (SEQ ID NO:230); GACCAATGAC (SEQ ID NO:231);
ACCAATGACT (SEQ ID NO:232); CCAATGACTT (SEQ ID NO:233);
CAATGACTTA (SEQ ID NO:234); AATGACTTAC (SEQ ID NO:235);
ATGACTTACA (SEQ ID NO:236); TGACTTACAA (SEQ ID NO:237);
GACTTACAAG (SEQ ID NO:238); ACTTACAAGG (SEQ ID NO:239);
CTTACAAGGC (SEQ ID NO:240); TTACAAGGCA (SEQ ID NO:241);
TACAAGGCAG (SEQ ID NO:242); ACAAGGCAGC (SEQ ID NO:243);
CAAGGCAGCT (SEQ ID NO:244); AAGGCAGCTG (SEQ ID NO:245);
AGGCAGCTGT (SEQ ID NO:246); GGCAGCTGTA (SEQ ID NO:247);
GCAGCTGTAG (SEQ ID NO:248); CAGCTGTAGA (SEQ ID NO:249);
AGCTGTAGAT (SEQ ID NO:250); GGTGTAGATC (SEQ ID NO:251);
CTGTAGATCT (SEQ ID NO:252); TGTAGATCTT (SEQ ID NO:253);
GTAGATCTTA (SEQ ID NO:254); TAGATCTTAG (SEQ ID NO:255);
AGATCTTAGC (SEQ ID NO:256); GATCTTAGCC (SEQ ID NO:257);
ATCTTAGCCA (SEQ ID NO:258); TCTTAGCCAC (SEQ ID NO:259);
CTTAGCCACT (SEQ ID NO:260); TTAGCCACTT (SEQ ID NO:261);
TAGCCACTTT (SEQ ID NO:262); AAGCACTTTT (SEQ ID NO:263);
GCCACTTTTT (SEQ ID NO:264); GCACTTTTTA (SEQ ID NO:265);
CACTTTTTAA (SEQ ID NO:266); ACTTTTTAAA (SEQ ID NO:267);
CTTTTTAAAA (SEQ ID NO:268); TTTTTAAAAA (SEQ ID NO:269);
TTTAAAGAA (SEQ ID NO:270); TTTAAAGAA (SEQ ID NO:271);
TTAAAGAAA (SEQ ID NO:272); TAAAGAAAAA (SEQ ID NO:273);
AAAAGAAAAG (SEQ ID NO:274); AAAGAAAAGG (SEQ ID NO:275);
AAGAAAAGGG (SEQ ID NO:276); AGAAAAGGGG (SEQ ID NO:277);
GAAAAGGGGG (SEQ ID NO:278); AAAAGGGGGG (SEQ ID NO:279);
AAAGGGGGGA (SEQ ID NO:280); AAGGGGGGAC (SEQ ID NO:281);
AGGGGGGACT (SEQ ID NO:282); GGGGGGACTG (SEQ ID NO:283);
GGGGGACTGG (SEQ ID NO:284); GGGGACTGGA (SEQ ID NO:285);
GGGACTGGAA (SEQ ID NO:286); GGACTGGAAG (SEQ ID NO:287);
GACTGGAAGG (SEQ ID NO:288); ACTGGAAGGG (SEQ ID NO:289);
CTGGAAGGGC (SEQ ID NO:290); TGGAAAGGGCT (SEQ ID NO:291);
GGAAGGGCTA (SEQ ID NO:292); GAAGGGCTAA (SEQ ID NO:293);
AAGGGCTAAT (SEQ ID NO:294); AGGGCTAATT (SEQ ID NO:295);
GGGCTAATTC (SEQ ID NO:296); GGCTAATTCA (SEQ ID NO:297);
GCTAATTCAC (SEQ ID NO:298); CTAATTCACT (SEQ ID NO:299);

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- 247 -

TAATTCACCTC (SEQ ID NO:300); AATTCACCTCC (SEQ ID NO:301);
ATTCACTCCC (SEQ ID NO:302); TTCACTCCCA (SEQ ID NO:303);
TCACTCCCAA (SEQ ID NO:304); CACTCCCAA (SEQ ID NO:305);
ACTCCCAAAG (SEQ ID NO:306); CTOCCAAAGA (SEQ ID NO:307);
TCCCAAAGAA (SEQ ID NO:308); CCCAAAGAAG (SEQ ID NO:309);
CCAAAGAAGA (SEQ ID NO:310); CAAAGAAGAC (SEQ ID NO:311);
AAAGAAGACA (SEQ ID NO:312); AAGAAGACAA (SEQ ID NO:313);
AGAAGACAAG (SEQ ID NO:314); GAAGACAAGA (SEQ ID NO:315);
AAGACAAGAT (SEQ ID NO:316); AGACAAGATA (SEQ ID NO:317);
GACAAGATAT (SEQ ID NO:318); ACAAGATATC (SEQ ID NO:319);
CAAGATATCC (SEQ ID NO:320); AAGATATCCT (SEQ ID NO:321);
AGATATCCTT (SEQ ID NO:322); GATATCCTTG (SEQ ID NO:323);
ATATCCTTGA (SEQ ID NO:324); TATCCTTGAT (SEQ ID NO:325);
ATCCTTGATC (SEQ ID NO:326); TCCTTGATCT (SEQ ID NO:327);
CCTTGATCTG (SEQ ID NO:328); CTTGATCTGT (SEQ ID NO:329);
TTGATCTGTG (SEQ ID NO:330); TGTCTGTGG (SEQ ID NO:331);
GATCTGTGGA (SEQ ID NO:332); ATCTGTGGAT (SEQ ID NO:333);
TCTGTGGATC (SEQ ID NO:334); CTGTGGATCT (SEQ ID NO:335);
TGTGGATCTA (SEQ ID NO:336); GTGGATCTAC (SEQ ID NO:337);
TGGATCTACC (SEQ ID NO:338); GATCTACCA (SEQ ID NO:339);
GATCTACCAC (SEQ ID NO:340); AGCTACCACA (SEQ ID NO:341);
TCTACCACAC (SEQ ID NO:342); CTACCACACA (SEQ ID NO:343);
TACCACACAC (SEQ ID NO:344); AGACACACA (SEQ ID NO:345);
CCACACACAA (SEQ ID NO:346); CACACACAAG (SEQ ID NO:347);
ACACACAAGG (SEQ ID NO:348); CACACAAGGC (SEQ ID NO:349);
ACACAAGGCT (SEQ ID NO:350); CACAAGGCTA (SEQ ID NO:351);
ACAAGGCTAC (SEQ ID NO:352); CAGGCTACT (SEQ ID NO:353);
AAGGCTACTT (SEQ ID NO:354); AGGCTACTTC (SEQ ID NO:355);
GGCTACTTCC (SEQ ID NO:356); GCTACTTCCC (SEQ ID NO:357);
CTACTTCCCT (SEQ ID NO:358); TACTTCCCTG (SEQ ID NO:359);
ACTTCCCTGA (SEQ ID NO:360); CTTCCCTGAT (SEQ ID NO:361);
TTCCCTGATT (SEQ ID NO:362); TCCCTGATTG (SEQ ID NO:363);
CCCTGATTGG (SEQ ID NO:364); CCTGATTGGC (SEQ ID NO:365);
CTGATTGGCA (SEQ ID NO:366); TCTATTGGCAG (SEQ ID NO:367);
GATTGGCAGA (SEQ ID NO:368); ATTGGCAGAA (SEQ ID NO:369);
TTGGCAGAAC (SEQ ID NO:370); TGGCAGAACT (SEQ ID NO:371);
GGCAGAACTA (SEQ ID NO:372); GCAGAACTAC (SEQ ID NO:373);
CAGAACTACA (SEQ ID NO:374); AGAACTACAC (SEQ ID NO:375);

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- 248 -

GAACTACACA (SEQ ID NO:376); AACTACACAC (SEQ ID NO:377);
ACTACACACC (SEQ ID NO:378); CTACACACCA (SEQ ID NO:379);
TACACACCAG (SEQ ID NO:380); ACACACCAGG (SEQ ID NO:381);
CACACCAGGG (SEQ ID NO:382); ACACCAGGGC (SEQ ID NO:383);
CACCAGGGCC (SEQ ID NO:384); ACCAGGGCCA (SEQ ID NO:385);
CCAGGGCCAG (SEQ ID NO:386); CAGGGCCAGG (SEQ ID NO:387);
AGGGCCAGGG (SEQ ID NO:388); GGGCCAGGGG (SEQ ID NO:389);
GGCCAGGGGT (SEQ ID NO:390); GCCAGGGGTC (SEQ ID NO:391);
CCAGGGGTCA (SEQ ID NO:392); CAGGGGTCAG (SEQ ID NO:393);
AGGGGTCAAG (SEQ ID NO:394); GGGGTCAAGT (SEQ ID NO:395);
GGGTCAAGTA (SEQ ID NO:396); GGTCAAGTAT (SEQ ID NO:397);
GTCAGATATC (SEQ ID NO:398); TCAGATATCC (SEQ ID NO:399);
CAGATATCCA (SEQ ID NO:400); AGATATCCAC (SEQ ID NO:401);
GATATCCACT (SEQ ID NO:402); ATATCCACTG (SEQ ID NO:403);
TATCCACTGA (SEQ ID NO:404); ATCCACTGAC (SEQ ID NO:405);
TCCACTGACC (SEQ ID NO:406); CCACTGACCT (SEQ ID NO:407);
CACTGACCTT (SEQ ID NO:408); ACTGACCTTT (SEQ ID NO:409);
CTGACCTTTG (SEQ ID NO:410); TGACCTTTGG (SEQ ID NO:411);
GACCTTTGGA (SEQ ID NO:412); ACCTTTGGAT (SEQ ID NO:413);
CCTTTGGATG (SEQ ID NO:414); CTTTGGATGG (SEQ ID NO:415);
TTTGGATGGT (SEQ ID NO:416); TTTGGATGGT (SEQ ID NO:417);
TGGATGGTGC (SEQ ID NO:418); GGTGGTGGCT (SEQ ID NO:419);
GATGGTGCTA (SEQ ID NO:420); ATGGTGCTAC (SEQ ID NO:421);
TGGTGCTACA (SEQ ID NO:422); GTTGCTACAA (SEQ ID NO:423);
GTGCTACAAG (SEQ ID NO:424); TGCTACAAGC (SEQ ID NO:425);
GCTACAAGCT (SEQ ID NO:426); CTACAAGCTA (SEQ ID NO:427);
TACAAGCTAG (SEQ ID NO:428); ACAAGCTAGT (SEQ ID NO:429);
CAAGCTAGTA (SEQ ID NO:430); AAGCTAGTAC (SEQ ID NO:431);
AGCTAGTACC (SEQ ID NO:432); GCTAGTACCA (SEQ ID NO:433);
CTAGTACCAG (SEQ ID NO:434); TAGTACCAGT (SEQ ID NO:435);
AGTACCAGTT (SEQ ID NO:436); GTACCAGTTG (SEQ ID NO:437);
TACCAGTTGA (SEQ ID NO:438); ACCAGTTGAG (SEQ ID NO:439);
CCAGTTGAGC (SEQ ID NO:440); CAGTTGAGCC (SEQ ID NO:441);
AGTTGAGCCA (SEQ ID NO:442); GTTGAGCCAG (SEQ ID NO:443);
TTGAGCCAGA (SEQ ID NO:444); TGAGCCAGAT (SEQ ID NO:445);
GAGCCAGATA (SEQ ID NO:446); AGCCAGATAA (SEQ ID NO:447);
GCCAGATAAG (SEQ ID NO:448); CCAGATAAGG (SEQ ID NO:449);
CAGATAAGGT (SEQ ID NO:450); AGATAAGGTA (SEQ ID NO:451);

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- 249 -

GATAAGGTAG (SEQ ID NO:452);	ATAAGGTAGA (SEQ ID NO:453);
TAAGGTAGAA (SEQ ID NO:454);	AAGGTAGAAG (SEQ ID NO:455);
AGGTAGAAGA (SEQ ID NO:456);	GGTAGAAGAG (SEQ ID NO:457);
GTAGAAGAGG (SEQ ID NO:458);	TAGAAGAGGC (SEQ ID NO:459);
AGAAGAGGCC (SEQ ID NO:460);	GAAGAGGCCA (SEQ ID NO:461);
AAGAGGCCAA (SEQ ID NO:462);	AGAGGCCAAT (SEQ ID NO:463);
GAGGCCAATA (SEQ ID NO:464);	AGGCCAATAA (SEQ ID NO:465);
GGCCAATAAA (SEQ ID NO:466);	GCCAATAAAG (SEQ ID NO:467);
CCAATAAAGG (SEQ ID NO:468);	CAATAAAGGA (SEQ ID NO:469);
AATAAAGGAG (SEQ ID NO:470);	ATAAAGGAGA (SEQ ID NO:471);
TAAAGGAGAG (SEQ ID NO:472);	AAAGGAGAGA (SEQ ID NO:473);
AAGGAGAGAA (SEQ ID NO:474);	AGGAGAGAAC (SEQ ID NO:475);
GGAGAGAAC A (SEQ ID NO:476);	GAGAGAACAC (SEQ ID NO:477);
AGAGAACACC (SEQ ID NO:478);	GAGAACACCA (SEQ ID NO:479);
AGAACACCAG (SEQ ID NO:480);	GAACACCAGC (SEQ ID NO:481);
AACACCAGCT (SEQ ID NO:482);	ACACCAGCTT (SEQ ID NO:483);
CACCAGCTTG (SEQ ID NO:484);	ACCAGCTTGT (SEQ ID NO:485);
CCAGCTTGTT (SEQ ID NO:486);	CAGCTTGTTA (SEQ ID NO:487);
AGCTTGTTAC (SEQ ID NO:488);	GCTTGTTACA (SEQ ID NO:489);
CTTGTTACAC (SEQ ID NO:490);	TTGTTACACC (SEQ ID NO:491);
TGTTACACCC (SEQ ID NO:492);	GTTACACCTT (SEQ ID NO:493);
TTACACCTTG (SEQ ID NO:494);	TACACCTTGT (SEQ ID NO:495);
ACACCTGTG (SEQ ID NO:496);	CACCTGTGA (SEQ ID NO:497);
ACCCTGTGAG (SEQ ID NO:498);	COCTGTGAGC (SEQ ID NO:499);
CCTGTGAGCC (SEQ ID NO:500);	CTGTGAGCCT (SEQ ID NO:501);
TGTGAGCCTG (SEQ ID NO:502);	GTGAGCCTGC (SEQ ID NO:503);
TGAGCCTGCA (SEQ ID NO:504);	GAGCCTGCAT (SEQ ID NO:505);
AGCCTGCATG (SEQ ID NO:506);	GCCTGCATGG (SEQ ID NO:507);
CCTGCATGGA (SEQ ID NO:508);	CTGCATGGAA (SEQ ID NO:509);
TGCATGGAAT (SEQ ID NO:510);	GCAATGGAATG (SEQ ID NO:511);
CATGGAATGG (SEQ ID NO:512);	ATGGAATGGA (SEQ ID NO:513);
TGGAATGGAT (SEQ ID NO:514);	GGAATGGATG (SEQ ID NO:515);
GAATGGATGA (SEQ ID NO:516);	AATGGATGAC (SEQ ID NO:517);
ATGGATGACC (SEQ ID NO:518);	TGGATGACCC (SEQ ID NO:519);
GGATGACCCT (SEQ ID NO:520);	GATGACCCTG (SEQ ID NO:521);
ATGACCCTGA (SEQ ID NO:522);	TGACCCTGAG (SEQ ID NO:523);
GACCCTGAGA (SEQ ID NO:524);	ACCCTGAGAG (SEQ ID NO:525);
CCCTGAGAGA (SEQ ID NO:526);	CCTGAGAGAG (SEQ ID NO:527);

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- 250 -

CTGAGAGAGA (SEQ ID NO:528); TGAGAGAGAA (SEQ ID NO:529);
GAGAGAGAAG (SEQ ID NO:530); AGAGAGAAAGT (SEQ ID NO:531);
GAGAGAAGTG (SEQ ID NO:532); AGAGAAGTGT (SEQ ID NO:533);
GAGAAGTGTT (SEQ ID NO:534); AGAAGTGTTA (SEQ ID NO:535);
GAAGTGTTAG (SEQ ID NO:536); AAGTGTTAGA (SEQ ID NO:537);
AGTGTTAGAG (SEQ ID NO:538); GTGTTAGAGT (SEQ ID NO:539);
TGTTAGAGTG (SEQ ID NO:540); GTTAGAGTGG (SEQ ID NO:541);
TTAGAGTGGA (SEQ ID NO:542); TAGAGTGGAG (SEQ ID NO:543);
AGAGTGGAGG (SEQ ID NO:544); GAGTGGAGGT (SEQ ID NO:545);
AGTGGAGGTT (SEQ ID NO:546); GTGGAGGTTT (SEQ ID NO:547);
TGGAGGTTTG (SEQ ID NO:548); GAGAGGTTTG (SEQ ID NO:549);
GAGGTTTGAC (SEQ ID NO:550); AGGTTTGACA (SEQ ID NO:551);
GGTTTGACAG (SEQ ID NO:552); GTTTGACAGC (SEQ ID NO:553);
TTTGACAGCC (SEQ ID NO:554); TTGACAGCCG (SEQ ID NO:555);
TGACAGCCGC (SEQ ID NO:556); GACAGCCGCC (SEQ ID NO:557);
ACAGCCGCCT (SEQ ID NO:558); CAGCCGCCTA (SEQ ID NO:559);
AGCCGCCTAG (SEQ ID NO:560); GCGCCCTAGC (SEQ ID NO:561);
CCGCCTAGCA (SEQ ID NO:562); CGCCTAGCAT (SEQ ID NO:563);
GCCTAGCATT (SEQ ID NO:564); CCTAGCATTT (SEQ ID NO:565);
CTAGCATTTT (SEQ ID NO:566); TAGCATTTCA (SEQ ID NO:567);
AGCATTTTCAT (SEQ ID NO:568); GCATTTTCATC (SEQ ID NO:569);
CATTTTCATCA (SEQ ID NO:570); ATTTTCATCAC (SEQ ID NO:571);
TTTCATCACG (SEQ ID NO:572); TTGATCACGT (SEQ ID NO:573);
TCATCACGTG (SEQ ID NO:574); CATCACGTGG (SEQ ID NO:575);
ATCACGTGGC (SEQ ID NO:576); TCGGTGGGCC (SEQ ID NO:577);
CACGTGGCCC (SEQ ID NO:578); AGGTGGCCCC (SEQ ID NO:579);
CGTGGCCCGA (SEQ ID NO:580); GTGGCCCGAG (SEQ ID NO:581);
TGGCCCGAGA (SEQ ID NO:582); GGGCCCGAGG (SEQ ID NO:583);
GCCCGAGAGC (SEQ ID NO:584); CCGGAGAGCT (SEQ ID NO:585);
CCGAGAGCTG (SEQ ID NO:586); CGAGAGCTGC (SEQ ID NO:587);
GAGAGCTGCA (SEQ ID NO:588); AGAGCTGCAT (SEQ ID NO:589);
GAGCTGCATC (SEQ ID NO:590); AGCTGCATCC (SEQ ID NO:591);
GCTGCATCCG (SEQ ID NO:592); CTGCATCCGG (SEQ ID NO:593);
TGCATCCGGA (SEQ ID NO:594); GCATCCGGAG (SEQ ID NO:595);
CATCCGGAGT (SEQ ID NO:596); ATCCGGAGTA (SEQ ID NO:597);
TCCGGAGTAC (SEQ ID NO:598); CGGAGTACTT (SEQ ID NO:599);
CGGAGTACTT (SEQ ID NO:600); GGAGTACTTC (SEQ ID NO:601);
GAGTACTTCA (SEQ ID NO:602); AGTACTTCAA (SEQ ID NO:603);

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- 251 -

GTACTTCAAG (SEQ ID NO:604); TACTTCAAGA (SEQ ID NO:605);
 ACTTCAAGAA (SEQ ID NO:606); CTTCAAGAAC (SEQ ID NO:607);
 TTCAAGAACT (SEQ ID NO:608); TCAAGAACTG (SEQ ID NO:609);
 CAAGAACTGC (SEQ ID NO:610); AAGAACTGCT (SEQ ID NO:611);
 AGAACTGCTG (SEQ ID NO:612); GAAGCTGCTGA (SEQ ID NO:613).

63. A method according to claim 57 wherein said deletion encompasses at least one of the following decanucleotides from the *nef* gene of HIV-1_{NL43}:

ACCAGCTTGT [SEQ ID NO:803]	CCAGCTTGT [SEQ ID NO:804]
CAGCTTGTTA [SEQ ID NO:805]	AGCTTGTAC [SEQ ID NO:806]
GCTTGTTACA [SEQ ID NO:807]	CTTGTTACAC [SEQ ID NO:808]
TTGTTACACC [SEQ ID NO:809]	TGTTACACCC [SEQ ID NO:810]
GTTACACCC [SEQ ID NO:811]	TTACACCCCTG [SEQ ID NO:812]
TACACCCCTG [SEQ ID NO:813]	ACACCCCTGTG [SEQ ID NO:814]
CACCCCTGTGA [SEQ ID NO:815]	ACCCCTGTGAG [SEQ ID NO:816]
CCCTGTGAGC [SEQ ID NO:817]	CCTGTGAGCC [SEQ ID NO:818]
CTGTGAGCCT [SEQ ID NO:819]	TGTGAGCCTG [SEQ ID NO:820]
GTGAGCCTGC [SEQ ID NO:821]	TGAGCCTGCA [SEQ ID NO:822]
GAGCCTGCAT [SEQ ID NO:823]	AGCCTGCATG [SEQ ID NO:824]
GCCTGCATGG [SEQ ID NO:825]	CCTGCATGGA [SEQ ID NO:826]
CTGCATGGAA [SEQ ID NO:827]	TGCATGGAAT [SEQ ID NO:828]
GCATGGAATG [SEQ ID NO:829]	CATGGAATGG [SEQ ID NO:830]
ATGGAATGGA [SEQ ID NO:831]	TGGAATGGAT [SEQ ID NO:832]
GGAATGGATG [SEQ ID NO:833]	GAATGGATGA [SEQ ID NO:834]
AATGGATGAC [SEQ ID NO:835]	ATGGATGACC [SEQ ID NO:836]
TGGATGACCC [SEQ ID NO:837]	GGATGACCCCT [SEQ ID NO:838]
GATGACCCCTG [SEQ ID NO:839]	ATGACCCCTGA [SEQ ID NO:840]
TGACCCCTGAG [SEQ ID NO:841]	

64. A method according to claim 57 wherein said deletion encompasses at least one of the following decanucleotides from the LTR region of HIV-1_{NL43}:

GCTTTTTGCC (SEQ ID NO:652);	CTTTTTGCCT (SEQ ID NO:653);
TTTTTGCCCTG (SEQ ID NO:654);	TTTTGCCTGT (SEQ ID NO:655);
TTTGCCCTGTA (SEQ ID NO:656);	TTGCCTGTAC (SEQ ID NO:657);
TGCCTGTACT (SEQ ID NO:658);	GCCTGTACTG (SEQ ID NO:659);
CCTGTACTGG (SEQ ID NO:660);	CTGTACTGGG (SEQ ID NO:661);
TGTACTGGGT (SEQ ID NO:662);	GTACTGGGTC (SEQ ID NO:663);

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- 252 -

TACTGGGTCT (SEQ ID NO:664); ACTGGGTCTC (SEQ ID NO:665);
 CTGGGTCTCT (SEQ ID NO:666); TGGGTCTCTC (SEQ ID NO:667);
 GGGTCTCTCT (SEQ ID NO:668); GGTCTCTCTG (SEQ ID NO:669);
 GTCTCTCTGG (SEQ ID NO:670); TCTCTCTGOT (SEQ ID NO:671);
 CTCTCTGGTT (SEQ ID NO:672); TCTCTGGTTA (SEQ ID NO:673);
 CTCTGGTTAG (SEQ ID NO:674); TCTCTGGTTA (SEQ ID NO:675);
 CTGGTTAGAC (SEQ ID NO:676); TGGTTAGACC (SEQ ID NO:677);
 GGTAGACCA (SEQ ID NO:678); GTTAGACCAG (SEQ ID NO:679);
 TTAGACCAGA (SEQ ID NO:680); TAGACCAGAT (SEQ ID NO:681);
 AGACCAGATC (SEQ ID NO:682); GAGCAGATCT (SEQ ID NO:683);
 ACCAGATCTG (SEQ ID NO:684); CAGATCTGTA (SEQ ID NO:685);
 CAGATCTGAG (SEQ ID NO:686); AGATCTGAGC (SEQ ID NO:687);
 GATCTGAGCC (SEQ ID NO:688); ATCTGAGCCT (SEQ ID NO:689);
 TCTGAGCCTG (SEQ ID NO:690); CTGAGCCTGG (SEQ ID NO:691);
 TGAGCCTGGG (SEQ ID NO:692); GAGCCTGGGA (SEQ ID NO:693);
 AGCCTGGGAG (SEQ ID NO:694); GCGTGGGAGC (SEQ ID NO:695);
 CCTGGGAGCT (SEQ ID NO:696); CTGGGAGCTC (SEQ ID NO:697);
 TGGGAGCTCT (SEQ ID NO:698); GGGAGCTCTC (SEQ ID NO:699);
 GGAGCTCTCT (SEQ ID NO:700); GAGCTCTCTG (SEQ ID NO:701);
 AGCTCTCTGG (SEQ ID NO:702); GCTCTCTGGC (SEQ ID NO:703);
 CTCTCTGGCT (SEQ ID NO:704); TCTCTGGCTA (SEQ ID NO:705);
 CTCTGGCTAA (SEQ ID NO:706); TCTGGCTAAC (SEQ ID NO:707);
 CTGGCTAACT (SEQ ID NO:708); TGGCTAACTA (SEQ ID NO:709);
 GGCTAACTAG (SEQ ID NO:710); GCTAACTAGG (SEQ ID NO:711);
 CTAAGCTAGG (SEQ ID NO:712); TAACTAGGGA (SEQ ID NO:713);
 AACTAGGGAA (SEQ ID NO:714); ACTAGGGAAAC (SEQ ID NO:715);
 CTAGGGAAACC (SEQ ID NO:716); TAGGGAAACCC (SEQ ID NO:717);
 AGGGAAACCA (SEQ ID NO:718); GGGAAACCCAC (SEQ ID NO:719);
 GGAACCCACT (SEQ ID NO:720); GAACCCACTG (SEQ ID NO:721);
 AACCCACTGC (SEQ ID NO:722); ACCCACTGCT (SEQ ID NO:723);
 CCCACTGCTT (SEQ ID NO:724); CCACTGCTTA (SEQ ID NO:725);
 CACTGCTTAA (SEQ ID NO:726); ACTGCTTAAG (SEQ ID NO:727);
 CTGCTTAAGC (SEQ ID NO:728); TGCTTAAGCC (SEQ ID NO:729);
 GCTTAAGCCT (SEQ ID NO:730); CTTAAGCCTC (SEQ ID NO:731);
 TTAAGCCTCA (SEQ ID NO:732); TAAGCCTCAA (SEQ ID NO:733);
 AAGCCTCAAT (SEQ ID NO:734); AGCCTCAATA (SEQ ID NO:735);
 GCCTCAATAA (SEQ ID NO:736); CCTCAATAAA (SEQ ID NO:737);
 CTCATAAAG (SEQ ID NO:738); TCAATAAAGC (SEQ ID NO:739);

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- 253 -

CAATAAAGCT (SEQ ID NO:740); AATAAAGCTT (SEQ ID NO:741);
 ATAAAGCTTG (SEQ ID NO:742); TAAAGCTTGC (SEQ ID NO:743);
 AAAGCTTGCC (SEQ ID NO:744); AAGCTTGCCCT (SEQ ID NO:745);
 AGCTTGCCCTT (SEQ ID NO:746); GCTTGCCCTTG (SEQ ID NO:747);
 CTTGCCTTGA (SEQ ID NO:748); TTGCCTTGAG (SEQ ID NO:749);
 TGCCTTGAGT (SEQ ID NO:750); GCCTTGAGTG (SEQ ID NO:751);
 CCTTGAGTGC (SEQ ID NO:752); CTTGAGTGCT (SEQ ID NO:753);
 TTGAGTGCTT (SEQ ID NO:754); TGAAGTGCTTC (SEQ ID NO:755);
 GAGTGCTTCA (SEQ ID NO:756); AGTGCTTCAA (SEQ ID NO:757);
 GTGCTTCAAG (SEQ ID NO:758); TGCTTCAAGT (SEQ ID NO:759);
 GCTTCAAGTA (SEQ ID NO:760); CTTCAAGTAG (SEQ ID NO:761);
 TTCAAGTAGT (SEQ ID NO:762); TCAAGTAGTG (SEQ ID NO:763);
 CAAGTAGTGT (SEQ ID NO:764); AAGTAGTG TG (SEQ ID NO:765);
 AGTAGTGTGT (SEQ ID NO:766); GTAGTGTGTG (SEQ ID NO:767);
 TAGTGTGTGC (SEQ ID NO:768); AGTGTGTGCC (SEQ ID NO:769);
 GTGTGTGCCC (SEQ ID NO:770); TGTGTGCCCC (SEQ ID NO:771);
 GTGTGCCCCG (SEQ ID NO:772); TGTGCCCCGTC (SEQ ID NO:773);
 GTGCCCCGTCT (SEQ ID NO:774); TGCCTGCTCTG (SEQ ID NO:775);
 GCCCGTCTGT (SEQ ID NO:776); CCGCTCTGTT (SEQ ID NO:777);
 CCGTCTGTTG (SEQ ID NO:778); CGTCTGTTGT (SEQ ID NO:779);
 GTCTGTTGTG (SEQ ID NO:780); TCTGTTGTGT (SEQ ID NO:781);
 CTGTTGTGTG (SEQ ID NO:782); TGTGTTGTGA (SEQ ID NO:783);
 GTTGTGTGAC (SEQ ID NO:784); TTGTGTGACT (SEQ ID NO:785);
 TGTGTGACTC (SEQ ID NO:786); GTGTGACTCT (SEQ ID NO:787);
 TGTGTGACTC (SEQ ID NO:788); GTGTGACTCT (SEQ ID NO:789);
 TGTGACTCTG (SEQ ID NO:790); GTGACTCTGG (SEQ ID NO:791);
 TGA CTCTGGT (SEQ ID NO:792); GACTCTGGTA (SEQ ID NO:793);
 ACTCTGGTAA (SEQ ID NO:794); CTCTGGTAAC (SEQ ID NO:795);
 TCTGGTAACT (SEQ ID NO:796); CTGGTAAC TA (SEQ ID NO:797);
 TGGTAACTAG (SEQ ID NO:798); GGTAACTAGA (SEQ ID NO:799).

65. A method according to claim 49 wherein said HIV-1 isolate has the identifying characteristics of HIV-1 isolate ECACC Accession No. V94101706 or HIV-1 isolate Accession No. ECACC V941031169 or HIV-1 isolate ECACC Accession No. V95031022.

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- 254 -

66. A method according to claim 49 wherein the HIV-1 isolate is reactive to antibodies to a glycoprotein of HIV-1, is capable of inducing an immune response of *gag*, *pol* and/or *env* and which is incapable of directing synthesis of a *nef* gene product or a full length *nef* gene product.

67. A method according to claim 66 wherein the glycoprotein is at least one of gp41-45, gp120 and/or gp160.

68. A method for obtaining a preparation of non-pathogenic HIV-1 from a biological sample, said method comprising co-culturing PBMCs from said biological sample from an individual putatively infected with said non-pathogenic HIV-1 with HIV-1 seronegative donor PBMCs depleted for CD8+ cells, harvesting the PBMCs and supernatant fluid every from about 5 to about 10 days and adding fresh medium with CD8+ depleted PBMCs with said fresh medium and isolating said virus from the supernatant fluid.

69. A method according to claim 68 wherein the seronegative PBMCs are pretreated with a cytokine for a time and under conditions sufficient to enhance HIV-1 replication.

70. A method according to claim 69 wherein the cytokine is M-CSF.

71. A method according to claim 68 or 69 or 70 wherein the HIV-1 seronegative donor PBMCs are first stimulated with PHA and/or IL-2.

72. A method according to claim 68 wherein the PBMCs from a putative infected individual are also CD8+ depleted prior to coculturing with seronegative donor PBMCs.

73. A method according to claim 68 or 72 wherein the cocultured cells are subjected to UV irradiation.

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- 255 -

74. A method for obtaining a preparation of non-pathogenic HIV-1 from a biological sample, said method comprising co-culturing monocytes from said biological sample from an individual putatively infected with said non-pathogenic HIV-1 with HIV-1 seronegative donor PBMCs depleted for CD8+ cells, harvesting the monocytes and PBMCs and supernatant fluid every from about 5 to about 10 days and adding fresh medium with CD8+ depleted PBMCs with said fresh medium and isolating said virus from the supernatant fluid.

75. A method according to claim 74 wherein the seronegative PBMCs are pretreated with a cytokine for a time and under conditions sufficient to enhance HIV-1 replication.

76. A method according to claim 75 wherein the cytokine is M-CSF.

77. A method according to claim 74 or 75 or 76 wherein the HIV-1 seronegative donor PBMCs are first stimulated with PHA and/or IL-2.

78. A method according to claim 74 wherein the monocytes from a putative infected individual are also CD8+ depleted prior to coculturing with seronegative donor PBMCs.

79. A method according to claim 74 or 78 wherein the cocultured cells are subjected to UV irradiation.

80. A method for identifying or screening for compounds capable of reducing or otherwise interfering with HIV-1 replication, said method comprising contacting a compound to be tested with a cell or cell extract containing or capable of containing a *nef* gene product fused to a reporter molecule capable of giving an identifiable signal and screening for a compound which inhibits said signal.

81. A method according to claim 80 wherein the compound is an antibody to *nef* gene product or a part thereof.

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- 256 -

82. A method according to claim 80 wherein the compound is a DNA targeting agent and inhibits transcription of the *nef* gene.
83. A compound capable of inhibiting *nef* gene product function or *nef* gene transcription.
84. A compound capable of inhibiting *nef* gene product function or *nef* gene transcription identified according to the method of claim 80 or 81 or 82.
85. A therapeutic composition useful for inhibiting or reducing productive infection by a pathogenic strain of HIV-1 and/or for vaccinating an individual against the development of AIDS or AIDS-related diseases, said composition comprising a non-pathogenic strain of HIV-1 according to any one of claims 1 to 16 and one or more pharmaceutical acceptable carriers and/or diluents.
86. A therapeutic composition according to claim 85 wherein said HIV-1 isolate comprises genetic material that directs expression of antisense or ribozyme nucleotide sequences which inhibit production of one or more proteins encoded by a pathogenic strain of HIV-1.
87. A viral isolate which:
- (i) is genetically or immunologically related to a pathogenic strain of HIV-1;
 - (ii) is substantially non-pathogenic in human subjects;
 - (iii) comprises a first nucleotide sequence constituting its genome which is capable of hybridising under medium stringency conditions to SEQ ID NO: 1 or a complementary form thereof; and
 - (iv) comprises a second nucleotide sequence within said first nucleotide sequence and which second nucleotide sequence directs expression of a mRNA molecule capable of inhibiting, reducing or otherwise down-regulating translation of a protein or polypeptide encoded by a pathogenic strain of HIV-1 or inhibit, reduce or otherwise down regulate operation of a non-protein encoding a region of a pathogenic strain of HIV-1.

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- 257 -

88. A viral isolate according to claim 87 wherein the targeted protein or polypeptide is selected from the list consisting of *gag* or *pol*.
89. A viral isolate according to claim 87 wherein the targeted protein or polypeptide is selected from the list consisting of *env* or *tat*.
90. A viral isolate according to claim 87 wherein the targeted protein or polypeptide is selected from the list consisting of *rev* or *vpr*.
91. A viral isolate according to claim 87 wherein the targeted protein or polypeptide is selected from the list consisting of *vpr*, *vif* or *nef*.
92. A viral isolate according to claim 87 wherein the targeted protein is *nef*.
93. A viral isolate according to claim 87 comprising a *nef* gene which substantially does not direct synthesis of amino acids 162 to 177 of Nef.
94. A method for determining the pathogenicity of an HIV-1 strain after said HIV-1 strain infects cells of an individual, said method comprising determining the presence of a deletion mutation in the genome of said HIV-1 wherein said deletion mutation results in said genome being unable to synthesize a polypeptide or protein from a pathogenic strain of HIV-1 or directing the synthesis of a truncated form of said polypeptide or protein wherein the presence of a such a mutation is indicative of the presence of a non-pathogenic strain of HIV-1.
95. A method according to claim 84 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43}.

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- 258 -

96. A method according to claim 94 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(i)	8830-8862;
	(ii)	9009-9035;
	(iii)	9019-9029; and
	(iv)	9033-9049.

97. A method according to claim 94 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(v)	9281-9371;
	(vi)	9281-9362;
	(vii)	9105-9224; and
	(viii)	9271-9370.

98. A method according to claim 94 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(ix)	8882-8928;
	(x)	8850-9006;
	(xi)	8792-9041; and
	(xii)	9112-9204.

99. A method according to claim 94 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(xiii)	9105-9224;
	(xiv)	9389-9395; and
	(xv)	9281-9366.

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- 259 -

100. A method according to claim 94 wherein said deletion encompasses at least one of the following decanucleotides from the *nef* gene of HIV-1_{ML43}:

ATGGGTGGCA (SEQ ID NO:2);	TGGGTGGCAA (SEQ ID NO:3);
GGGTGGCAAG (SEQ ID NO:4);	GGTGGCAAGT (SEQ ID NO:5);
GTGGCAAGTG (SEQ ID NO:6);	TGGCAAGTGG (SEQ ID NO:7);
GGCAAGTGGT (SEQ ID NO:8);	GCAAGTGGTC (SEQ ID NO:9);
CAAGTGGTCA (SEQ ID NO:10);	AAGTGGTCAA (SEQ ID NO:11);
AGTGGTCAAA (SEQ ID NO:12);	GTGGTCAAAA (SEQ ID NO:13);
TGGTCAAAA (SEQ ID NO:14);	GGTCAAAAAG (SEQ ID NO:15);
GTCAAAAAGT (SEQ ID NO:16);	TCAAAAGTA (SEQ ID NO:17);
CAAAAAGTAG (SEQ ID NO:18);	AAAAAGTAGT (SEQ ID NO:19);
AAAAGTAGTG (SEQ ID NO:20);	AAAGTAGTGT (SEQ ID NO:21);
AAGTAGTGTG (SEQ ID NO:22);	AGTAGTGTGA (SEQ ID NO:23);
GTAGTGTGAT (SEQ ID NO:24);	TAGTGTGATT (SEQ ID NO:25);
AGTGTGATTG (SEQ ID NO:26);	GTGTGATTGG (SEQ ID NO:27);
TGTGATTGGA (SEQ ID NO:28);	GTGATTGGAT (SEQ ID NO:29);
TGATTGGATG (SEQ ID NO:30);	GATTGGATGG (SEQ ID NO:31);
ATTGGATGGC (SEQ ID NO:32);	TGGATGGGCC (SEQ ID NO:33);
TGGATGGCCT (SEQ ID NO:34);	GGATGGCCTG (SEQ ID NO:35);
GATGGCCTGC (SEQ ID NO:36);	ATGGCCTGCT (SEQ ID NO:37);
TGGCCTGCTG (SEQ ID NO:38);	GGGCTGCTGT (SEQ ID NO:39);
GCCTGCTGTA (SEQ ID NO:40);	CCTGCTGTAA (SEQ ID NO:41);
CTGCTGTAAG (SEQ ID NO:42);	TGCTGTAAGG (SEQ ID NO:43);
GCTGTAAGGG (SEQ ID NO:44);	CTGTAAGGGA (SEQ ID NO:45);
TGTAAGGGAA (SEQ ID NO:46);	GTAAGGGAAA (SEQ ID NO:47);
TAAGGGAAAG (SEQ ID NO:48);	AAGGGAAAGA (SEQ ID NO:49);
AGGGAAAGAA (SEQ ID NO:50);	GGGAAAGAAT (SEQ ID NO:51);
GGAAAGAATG (SEQ ID NO:52);	GAAAGAATGA (SEQ ID NO:53);
AAAGAATGAG (SEQ ID NO:54);	AAGAATGAGA (SEQ ID NO:55);
AGAATGAGAC (SEQ ID NO:56);	GAATGAGACG (SEQ ID NO:57);
AATGAGACGA (SEQ ID NO:58);	ATGAGACGAG (SEQ ID NO:59);
TGAGACGAGC (SEQ ID NO:60);	GAGACGAGCT (SEQ ID NO:61);
AGACGAGCTG (SEQ ID NO:62);	GACGAGCTGA (SEQ ID NO:63);
ACGAGCTGAG (SEQ ID NO:64);	CGAGCTGAGC (SEQ ID NO:65);
GAGCTGAGCC (SEQ ID NO:66);	AGCTGAGCCA (SEQ ID NO:67);
GCTGAGCCAG (SEQ ID NO:68);	CTGAGCCAGC (SEQ ID NO:69);
TGAGCCAGCA (SEQ ID NO:70);	GAGCCAGCAG (SEQ ID NO:71);

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- 260 -

AGCCAGCAGC (SEQ ID NO:72);	GCCAGCAGCA (SEQ ID NO:73);
CCAGCAGCAG (SEQ ID NO:74);	CAGCAGCAGA (SEQ ID NO:75);
AGCAGCAGAT (SEQ ID NO:76);	GCAGCAGATG (SEQ ID NO:77);
CAGCAGATGG (SEQ ID NO:78);	AGCAGATGGG (SEQ ID NO:79);
GCAGATGGGG (SEQ ID NO:80);	CAGATGGGGT (SEQ ID NO:81);
AGATGGGGTG (SEQ ID NO:82);	GATGGGGTGG (SEQ ID NO:83);
ATGGGGTGGG (SEQ ID NO:84);	TGGGGTGGGA (SEQ ID NO:85);
GGGGTGGGAG (SEQ ID NO:86);	GGGTGGGAGC (SEQ ID NO:87);
GGTGGGAGCA (SEQ ID NO:88);	GTGGGAGCAG (SEQ ID NO:89);
TGGGAGCAGT (SEQ ID NO:90);	GGGAGCAGTA (SEQ ID NO:91);
GGAGCAGTAT (SEQ ID NO:92);	GAGCAGTATC (SEQ ID NO:93);
AGCAGTATCT (SEQ ID NO:94);	GCAGTATCTC (SEQ ID NO:95);
CAGTATCTCG (SEQ ID NO:96);	AGTATCTCGA (SEQ ID NO:97);
GTATCTCGAG (SEQ ID NO:98);	TATCTCGAGA (SEQ ID NO:99);
ATCTCGAGAC (SEQ ID NO:100);	TCTCGAGACC (SEQ ID NO:101);
CTCGAGACCT (SEQ ID NO:102);	TOGAGACCTA (SEQ ID NO:103);
CGAGACCTAG (SEQ ID NO:104);	GAGACCTAGA (SEQ ID NO:105);
AGACCTAGAA (SEQ ID NO:106);	GAGCTAGAAA (SEQ ID NO:107);
ACCTAGAAAA (SEQ ID NO:108);	CCTAGAAAAA (SEQ ID NO:109);
CTAGAAAAAC (SEQ ID NO:110);	TAGAAAAACA (SEQ ID NO:111);
AGAAAAACAT (SEQ ID NO:112);	GAAAAACATG (SEQ ID NO:113);
AAAAACATGG (SEQ ID NO:114);	AAACATGGGA (SEQ ID NO:115);
AAACATGGAG (SEQ ID NO:116);	AACATGGAGC (SEQ ID NO:117);
ACATGGAGCA (SEQ ID NO:118);	CATGGAGCAA (SEQ ID NO:119);
ATGGAGCAAT (SEQ ID NO:120);	TGGAGCAATC (SEQ ID NO:121);
GGAGCAATCA (SEQ ID NO:122);	GAGCAATCAC (SEQ ID NO:123);
AGCAATCACA (SEQ ID NO:124);	GCAATCACAA (SEQ ID NO:125);
CAATCACAAG (SEQ ID NO:126);	AATCACAGT (SEQ ID NO:127);
ATCACAAGTA (SEQ ID NO:128);	TCACAAGTAG (SEQ ID NO:129);
CACAAGTAGC (SEQ ID NO:130);	ACAAGTAGCA (SEQ ID NO:131);
CAAGTAGCAA (SEQ ID NO:132);	AAGTAGCAAT (SEQ ID NO:133);
AGTAGCAATA (SEQ ID NO:134);	GTAGCAATAC (SEQ ID NO:135);
TAGCAATACA (SEQ ID NO:136);	AGCAATACAG (SEQ ID NO:137);
GCAATACAGC (SEQ ID NO:138);	CAATACAGCA (SEQ ID NO:139);
AATACAGCAG (SEQ ID NO:140);	ATACAGCAGC (SEQ ID NO:141);
TACAGCAGCT (SEQ ID NO:142);	ACAGCAGCTA (SEQ ID NO:143);
CAGCAGCTAA (SEQ ID NO:144);	AGCAGCTAAC (SEQ ID NO:145);
GCAGCTAACA (SEQ ID NO:146);	CAGCTAACAA (SEQ ID NO:147);

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- 261 -

AGCTAACAAT (SEQ ID NO:148); GCTAACAATG (SEQ ID NO:149);
CTAACAATGC (SEQ ID NO:150); TAACAATGCT (SEQ ID NO:151);
AACAAATGCTG (SEQ ID NO:152); ACAATGCTGC (SEQ ID NO:153);
CAATGCTGCT (SEQ ID NO:154); AATGCTGCTT (SEQ ID NO:155);
ATGCTGCTTG (SEQ ID NO:156); TGCTGCTTGT (SEQ ID NO:157);
GCTGCTTGTT (SEQ ID NO:158); CTGCTTGTTG (SEQ ID NO:159);
TGCTTGTTGCC (SEQ ID NO:160); GCTTGTTGCC (SEQ ID NO:161);
CTTGTTGCCCTG (SEQ ID NO:162); TTGTTGCCCTGG (SEQ ID NO:163);
TGTGCTGGC (SEQ ID NO:164); GTGCTGGCCT (SEQ ID NO:165);
TGCCTGGCTA (SEQ ID NO:166); GCCTGGCTAG (SEQ ID NO:167);
CCTGGCTAGA (SEQ ID NO:168); CTGGCTAGAA (SEQ ID NO:169);
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GCTAGAAGCA (SEQ ID NO:172); CTAGAAGCAC (SEQ ID NO:173);
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CACAAGAGGA (SEQ ID NO:180); ACAAGAGGAG (SEQ ID NO:181);
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AGAGGAGGAA (SEQ ID NO:184); GAGGAGGAAG (SEQ ID NO:185);
AGGAGGAAGA (SEQ ID NO:186); GGAGGAAGAG (SEQ ID NO:187);
GAGGAAGAGG (SEQ ID NO:188); AGGAAGAGGT (SEQ ID NO:189);
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AAGAGGTGGG (SEQ ID NO:192); AGAGGTGGGT (SEQ ID NO:193);
GAGGTGGGTT (SEQ ID NO:194); AGGTGGGTTT (SEQ ID NO:195);
GGTGGGTTTT (SEQ ID NO:196); GTGGGTTTTT (SEQ ID NO:197);
TGGGTTTTTCC (SEQ ID NO:198); GGTTTTTTCCA (SEQ ID NO:199);
GGTTTTTCCAG (SEQ ID NO:200); GTTTTTCCAGT (SEQ ID NO:201);
TTTTCCAGTC (SEQ ID NO:202); TTTCAGTCA (SEQ ID NO:203);
TTCCAGTCAC (SEQ ID NO:204); TCCAGTCACA (SEQ ID NO:205);
CCAGTCACAC (SEQ ID NO:206); CAGTCACACC (SEQ ID NO:207);
AGTCACACCT (SEQ ID NO:208); GTCACACCTC (SEQ ID NO:209);
TCACACCTCA (SEQ ID NO:210); CACACCTCAG (SEQ ID NO:211);
ACACCTCAGG (SEQ ID NO:212); CACCTCAGGT (SEQ ID NO:213);
ACCTCAGGTA (SEQ ID NO:214); CCTCAGGTAC (SEQ ID NO:215);
CTCAGGTACC (SEQ ID NO:216); TCAGGTACCT (SEQ ID NO:217);
CAGGTACCTT (SEQ ID NO:218); AGGTACCTTT (SEQ ID NO:219);
GGTACCTTTA (SEQ ID NO:220); GTACCTTTAA (SEQ ID NO:221);
TACCTTTAAG (SEQ ID NO:222); ACCTTTAAGA (SEQ ID NO:223);

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- 262 -

CCTTTAAGAC (SEQ ID NO:224);	CTTTAAGACC (SEQ ID NO:225);
TTTAAGACCA (SEQ ID NO:226);	TTAAGACCAA (SEQ ID NO:227);
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AGACCAATGA (SEQ ID NO:230);	GACCAATGAC (SEQ ID NO:231);
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CAATGACTTA (SEQ ID NO:234);	AATGACTTAC (SEQ ID NO:235);
ATGACTTACA (SEQ ID NO:236);	TGACTTACAA (SEQ ID NO:237);
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CAAGGCAGCT (SEQ ID NO:244);	AAGGCAGCTG (SEQ ID NO:245);
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CACTTTTTAA (SEQ ID NO:266);	ACTTTTTAAA (SEQ ID NO:267);
CTTTTTAAAA (SEQ ID NO:268);	TTTTTAAAG (SEQ ID NO:269);
TTTTAAAAGA (SEQ ID NO:270);	TTTAAAAGAA (SEQ ID NO:271);
TTAAAAGAAA (SEQ ID NO:272);	TAAAAGAAAA (SEQ ID NO:273);
AAAAGAAAAG (SEQ ID NO:274);	AAAGAAAAGG (SEQ ID NO:275);
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GACTGGAAGG (SEQ ID NO:288);	ACTGGAAGGG (SEQ ID NO:289);
CTGGAAGGGC (SEQ ID NO:290);	TGGAAGGGCT (SEQ ID NO:291);
GGAAGGGCTA (SEQ ID NO:292);	GAAGGGCTAA (SEQ ID NO:293);
AAGGGCTAAT (SEQ ID NO:294);	AGGGCTAATT (SEQ ID NO:295);
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GCTAATTCAC (SEQ ID NO:298);	CTAATTCACT (SEQ ID NO:299);

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- 263 -

TAATTCACTC (SEQ ID NO:300); AATTCACTCC (SEQ ID NO:301);
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TCCCAAAGAA (SEQ ID NO:308); CCCAAAGAAG (SEQ ID NO:309);
CCAAAGAAGA (SEQ ID NO:310); CAAAGAAGAC (SEQ ID NO:311);
AAAGAAGACA (SEQ ID NO:312); AAGAAGACAA (SEQ ID NO:313);
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CAAGATATCC (SEQ ID NO:320); AAGATATCCT (SEQ ID NO:321);
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CAGAACTACA (SEQ ID NO:374); AGAACTACAC (SEQ ID NO:375);

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- 264 -

GA ACTACACA (SEQ ID NO:376); AACTACACAC (SEQ ID NO:377);
ACTACACACC (SEQ ID NO:378); CTACACACCA (SEQ ID NO:379);
TACACACCAG (SEQ ID NO:380); ACACACCAGG (SEQ ID NO:381);
CACACCAGGG (SEQ ID NO:382); ACACCAGGGC (SEQ ID NO:383);
CACCAGGGCC (SEQ ID NO:384); ACCAGGGCCA (SEQ ID NO:385);
CCAGGGCCAG (SEQ ID NO:386); CAGGGCCAGG (SEQ ID NO:387);
AGGGCCAGGG (SEQ ID NO:388); GGGCCAGGGG (SEQ ID NO:389);
GGCCAGGGGT (SEQ ID NO:390); GCCAGGGGTC (SEQ ID NO:391);
CCAGGGGTCA (SEQ ID NO:392); CAGGGGTCAG (SEQ ID NO:393);
AGGGGTCAGA (SEQ ID NO:394); GGGGTCAGAT (SEQ ID NO:395);
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CAGATATCCA (SEQ ID NO:400); AGATATCCAC (SEQ ID NO:401);
GATATCCACT (SEQ ID NO:402); ATATCCACTG (SEQ ID NO:403);
TATCCACTGA (SEQ ID NO:404); ATCCACTGAC (SEQ ID NO:405);
TCCACTGACC (SEQ ID NO:406); CCACTGACCT (SEQ ID NO:407);
CACTGACCTT (SEQ ID NO:408); ACTGACCTTT (SEQ ID NO:409);
CTGACCTTTG (SEQ ID NO:410); TGACCTTTGG (SEQ ID NO:411);
GACCTTTGGA (SEQ ID NO:412); ACCTTTGGAT (SEQ ID NO:413);
CCTTTGGATG (SEQ ID NO:414); CTTTGGATGG (SEQ ID NO:415);
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TGGTGCTACA (SEQ ID NO:422); GGTGCTACAA (SEQ ID NO:423);
GTGCTACAAG (SEQ ID NO:424); TGCTACAAGC (SEQ ID NO:425);
GCTACAAGCT (SEQ ID NO:426); CTACAAGCTA (SEQ ID NO:427);
TACAAGCTAG (SEQ ID NO:428); ACAAGCTAGT (SEQ ID NO:429);
CAAGCTAGTA (SEQ ID NO:430); AAGCTAGTAC (SEQ ID NO:431);
AGCTAGTACC (SEQ ID NO:432); GCTAGTACCA (SEQ ID NO:433);
CTAGTACCAG (SEQ ID NO:434); TAGTACCAGT (SEQ ID NO:435);
AGTACCAGTT (SEQ ID NO:436); GTACCAGTTG (SEQ ID NO:437);
TACCAGTTGA (SEQ ID NO:438); ACCAGTTGAG (SEQ ID NO:439);
CCAGTTGAGC (SEQ ID NO:440); CAGTTGAGCC (SEQ ID NO:441);
AGTTGAGCCA (SEQ ID NO:442); GTTGAGCCAG (SEQ ID NO:443);
TTGAGCCAGA (SEQ ID NO:444); TGAGCCAGAT (SEQ ID NO:445);
GAGCCAGATA (SEQ ID NO:446); AGCCAGATAA (SEQ ID NO:447);
GCCAGATAAG (SEQ ID NO:448); CCAGATAAGG (SEQ ID NO:449);
CAGATAAGGT (SEQ ID NO:450); AGATAAGGTA (SEQ ID NO:451);

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- 265 -

GATAAGGTAG (SEQ ID NO:452); ATAAGGTAGA (SEQ ID NO:453);
TAAGGTAGAA (SEQ ID NO:454); AAGGTAGAAG (SEQ ID NO:455);
AGGTAGAAGA (SEQ ID NO:456); GGTAGAAGAG (SEQ ID NO:457);
GTAGAAGAGG (SEQ ID NO:458); TAGAAGAGGC (SEQ ID NO:459);
AGAAGAGGCC (SEQ ID NO:460); GAAGAGGCCA (SEQ ID NO:461);
AAGAGGCCAA (SEQ ID NO:462); AGAGGCCAAT (SEQ ID NO:463);
GAGGCCAATA (SEQ ID NO:464); AGGCCAATAA (SEQ ID NO:465);
GGCCAATAAA (SEQ ID NO:466); GCCAATAAAG (SEQ ID NO:467);
CCAATAAAGG (SEQ ID NO:468); CAATAAAGGA (SEQ ID NO:469);
AATAAAGGAG (SEQ ID NO:470); ATAAAGGAGA (SEQ ID NO:471);
TAAAGGAGAG (SEQ ID NO:472); AAAGGAGAGA (SEQ ID NO:473);
AAGGAGAGAA (SEQ ID NO:474); AGGAGAGAAC (SEQ ID NO:475);
GGAGAGAACA (SEQ ID NO:476); GAGAGAACAC (SEQ ID NO:477);
AGAGAACACC (SEQ ID NO:478); GAGAACACCA (SEQ ID NO:479);
AGAACACCAG (SEQ ID NO:480); GACACCAGC (SEQ ID NO:481);
AACACCAGCT (SEQ ID NO:482); ACACCAGCTT (SEQ ID NO:483);
CACCAGCTTG (SEQ ID NO:484); ACCAGCTTGT (SEQ ID NO:485);
CCAGCTTGTT (SEQ ID NO:486); CAGCTTGTTA (SEQ ID NO:487);
AGCTTGTTAC (SEQ ID NO:488); GCTTGTTACA (SEQ ID NO:489);
CTTGTTACAC (SEQ ID NO:490); TTGTTACACC (SEQ ID NO:491);
TGTTACACCC (SEQ ID NO:492); GTTACACCCCT (SEQ ID NO:493);
TTACACCCCTG (SEQ ID NO:494); TAGACCCCTGT (SEQ ID NO:495);
ACACCCCTGTG (SEQ ID NO:496); CACCCCTGTGA (SEQ ID NO:497);
ACCCTGTGAG (SEQ ID NO:498); CCCTGTGAGC (SEQ ID NO:499);
CCTGTGAGCC (SEQ ID NO:500); CTGTGAGCCT (SEQ ID NO:501);
TGTGAGCCTG (SEQ ID NO:502); GTGAGCCTGC (SEQ ID NO:503);
TGAGCCTGCA (SEQ ID NO:504); GAGCCTGCAT (SEQ ID NO:505);
AGCCTGCATG (SEQ ID NO:506); GCCTGCATGG (SEQ ID NO:507);
CCTGCATGGA (SEQ ID NO:508); CTGCATGGAA (SEQ ID NO:509);
TGCATGGAAT (SEQ ID NO:510); GCATGGAATG (SEQ ID NO:511);
CATGGAATGG (SEQ ID NO:512); ATGGAATGGA (SEQ ID NO:513);
TGGAATGGAT (SEQ ID NO:514); GGAATGGATG (SEQ ID NO:515);
GAATGGATGA (SEQ ID NO:516); AATGGATGAC (SEQ ID NO:517);
ATGGATGACC (SEQ ID NO:518); TGGATGACCC (SEQ ID NO:519);
GGATGACCCT (SEQ ID NO:520); GATGACCCTG (SEQ ID NO:521);
ATGACCCTGA (SEQ ID NO:522); TGACCCTGAG (SEQ ID NO:523);
GACCCTGAGA (SEQ ID NO:524); ACCCTGAGAG (SEQ ID NO:525);
CCCTGAGAGA (SEQ ID NO:526); CCTGAGAGAG (SEQ ID NO:527);

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- 266 -

CTGAGAGAGA (SEQ ID NO:528); TGAGAGAGAA (SEQ ID NO:529);
GAGAGAGAAG (SEQ ID NO:530); AGAGAGAAAGT (SEQ ID NO:531);
GAGAGAAGTG (SEQ ID NO:532); AGAGAAGTGT (SEQ ID NO:533);
GAGAAGTGTT (SEQ ID NO:534); AGAAGTGTTA (SEQ ID NO:535);
GAAGTGTTAG (SEQ ID NO:536); AAGTGTTAGA (SEQ ID NO:537);
AGTGTTAGAG (SEQ ID NO:538); GTGTTAGAGT (SEQ ID NO:539);
TGTTAGAGTG (SEQ ID NO:540); GTTAGAGTGG (SEQ ID NO:541);
TTAGAGTGGG (SEQ ID NO:542); TAGAGTGGAG (SEQ ID NO:543);
AGAGTGGAGG (SEQ ID NO:544); GAGTGGAGGT (SEQ ID NO:545);
AGTGGAGGTT (SEQ ID NO:546); GTGGAGGTTT (SEQ ID NO:547);
TGGAGGTTTG (SEQ ID NO:548); GGAGGTTTGA (SEQ ID NO:549);
GAGGTTTGAC (SEQ ID NO:550); AGGTTTGACA (SEQ ID NO:551);
GGTTTGACAG (SEQ ID NO:552); GTTGACAGC (SEQ ID NO:553);
TTTGACAGCC (SEQ ID NO:554); TTGACAGCCG (SEQ ID NO:555);
TGACAGCCGC (SEQ ID NO:556); GACAGCCGCC (SEQ ID NO:557);
ACAGCCGCCT (SEQ ID NO:558); CAGCCGCCTA (SEQ ID NO:559);
AGCCGCCTAG (SEQ ID NO:560); GCGCCCTAGC (SEQ ID NO:561);
CGCCCTAGCA (SEQ ID NO:562); CGCCTAGCAT (SEQ ID NO:563);
GCCTAGCATT (SEQ ID NO:564); CGTAGCATTT (SEQ ID NO:565);
CTAGCATTTT (SEQ ID NO:566); TAGCATTTCA (SEQ ID NO:567);
AGCATTTTCAT (SEQ ID NO:568); GCATTTTCATC (SEQ ID NO:569);
CATTTTCATCA (SEQ ID NO:570); ATTTTCATCAC (SEQ ID NO:571);
TTTCATCACG (SEQ ID NO:572); TTCATCACGT (SEQ ID NO:573);
TCATCACGTG (SEQ ID NO:574); CATCACGTGG (SEQ ID NO:575);
ATCACGTGGC (SEQ ID NO:576); TCACGTGGCC (SEQ ID NO:577);
CACGTGGCCC (SEQ ID NO:578); AGGTGGCCCC (SEQ ID NO:579);
CGTGGCCCCG (SEQ ID NO:580); GTGGCCCCGAG (SEQ ID NO:581);
TGGCCCCGAG (SEQ ID NO:582); GGCCCCGAGAG (SEQ ID NO:583);
GCCCCGAGAGC (SEQ ID NO:584); CCGGAGAGCT (SEQ ID NO:585);
CCGAGAGCTG (SEQ ID NO:586); CGAGAGCTGC (SEQ ID NO:587);
GAGAGCTGCA (SEQ ID NO:588); AGAGCTGCAT (SEQ ID NO:589);
GAGCTGCATC (SEQ ID NO:590); AGCTGCATCC (SEQ ID NO:591);
GCTGCATCCG (SEQ ID NO:592); CTGCATCCGG (SEQ ID NO:593);
TGCATCCGGA (SEQ ID NO:594); GCATCCGGAG (SEQ ID NO:595);
CATCCGGAGT (SEQ ID NO:596); ATCCGGAGTA (SEQ ID NO:597);
TCCGGAGTAC (SEQ ID NO:598); CCGGAGTACT (SEQ ID NO:599);
CGGAGTACTT (SEQ ID NO:600); GGAGTACTTC (SEQ ID NO:601);
GAGTACTTCA (SEQ ID NO:602); AGTACTTCAA (SEQ ID NO:603);

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- 267 -

GTACTTCAAG (SEQ ID NO:604); TACTTCAAGA (SEQ ID NO:605);
 ACTTCAAGAA (SEQ ID NO:606); CTTCAAGAAC (SEQ ID NO:607);
 TTCAAGAACT (SEQ ID NO:608); TCAAGAACTG (SEQ ID NO:609);
 CAAGAACTGC (SEQ ID NO:610); AAGAACTGCT (SEQ ID NO:611);
 AGAACTGCTG (SEQ ID NO:612); GAACTGCTGA (SEQ ID NO:613).

101. A method according to claim 94 wherein said deletion encompasses at least one of the following decanucleotides from the *nef* gene of HIV-1_{NL43}:

ACCAGCTTGT [SEQ ID NO:803]	CCAGCTTGTT [SEQ ID NO:804]
CAGCTTGTTA [SEQ ID NO:805]	AGCTTGTTAC [SEQ ID NO:806]
GCTTGTTACA [SEQ ID NO:807]	CTTGTTACAC [SEQ ID NO:808]
TTGTTACACC [SEQ ID NO:809]	TGTTACACCC [SEQ ID NO:810]
GTTACACCCT [SEQ ID NO:811]	TTACACCCTG [SEQ ID NO:812]
TACACCCTGT [SEQ ID NO:813]	ACACCCTGTG [SEQ ID NO:814]
CACCCTGTGA [SEQ ID NO:815]	ACCTGTGAG [SEQ ID NO:816]
CCCTGTGAGC [SEQ ID NO:817]	CCTGTGAGCC [SEQ ID NO:818]
CTGTGAGCCT [SEQ ID NO:819]	TGTGAGCCTG [SEQ ID NO:820]
GTGAGCCTGC [SEQ ID NO:821]	TGAGCCTGCA [SEQ ID NO:822]
GAGCCTGCAT [SEQ ID NO:823]	AGCCTGCATG [SEQ ID NO:824]
GCCTGCATGG [SEQ ID NO:825]	CCTGCATGGA [SEQ ID NO:826]
CTGCATGGA [SEQ ID NO:827]	TGCATGGAAT [SEQ ID NO:828]
GCATGGAATG [SEQ ID NO:829]	CATGGAATGG [SEQ ID NO:830]
ATGGAATGGA [SEQ ID NO:831]	TGGAATGGAT [SEQ ID NO:832]
GGAATGGATG [SEQ ID NO:833]	GAATGGATGA [SEQ ID NO:834]
AATGGATGAC [SEQ ID NO:835]	ATGGATGACC [SEQ ID NO:836]
TGGATGACCC [SEQ ID NO:837]	GGATGACCCT [SEQ ID NO:838]
GATGACCCTG [SEQ ID NO:839]	ATGACCCTGA [SEQ ID NO:840]
TGACCCTGAG [SEQ ID NO:841]	

102. A method according to claim 94 wherein said deletion encompasses at least one of the following decanucleotides from the LTR region of HIV-1_{NL43}:

GCTTTTGGCC (SEQ ID NO:652);	CTTTTGCCT (SEQ ID NO:653);
TTTTTGCCTG (SEQ ID NO:654);	TTTTGCCTGT (SEQ ID NO:655);
TTTGCCTGTA (SEQ ID NO:656);	TTGCCTGTAC (SEQ ID NO:657);
TGCCTGTACT (SEQ ID NO:658);	GCCTGTACTG (SEQ ID NO:659);
CCTGTACTGG (SEQ ID NO:660);	CTGTACTGGG (SEQ ID NO:661);
TGTACTGGCT (SEQ ID NO:662);	GTACTGGGTC (SEQ ID NO:663);

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- 268 -

TACTGGGTCT (SEQ ID NO:664); ACTGGGTCTC (SEQ ID NO:665);
CTGGGTCTCT (SEQ ID NO:666); TGGGTCTCTC (SEQ ID NO:667);
GGGTCTCTCT (SEQ ID NO:668); GGTCTCTCTG (SEQ ID NO:669);
GTCTCTCTGG (SEQ ID NO:670); TCTCTCTGGT (SEQ ID NO:671);
CTCTCTGGTT (SEQ ID NO:672); TCTCTGGTTA (SEQ ID NO:673);
CTCTGGTTAG (SEQ ID NO:674); TCTCTGGTTA (SEQ ID NO:675);
CTGGTTAGAC (SEQ ID NO:676); TGOTTAGACC (SEQ ID NO:677);
GGTTAGACCA (SEQ ID NO:678); GTTAGACCAG (SEQ ID NO:679);
TTAGACCAGA (SEQ ID NO:680); TAGACCAGAT (SEQ ID NO:681);
AGACCAGATC (SEQ ID NO:682); GACCAGATCT (SEQ ID NO:683);
ACCAGATCTG (SEQ ID NO:684); CCAGATCTGA (SEQ ID NO:685);
CAGATCTGAG (SEQ ID NO:686); AGATCTGAGC (SEQ ID NO:687);
GATCTGAGCC (SEQ ID NO:688); ATCTGAGCCT (SEQ ID NO:689);
TCTGAGCCTG (SEQ ID NO:690); CTGAGCCTGG (SEQ ID NO:691);
TGAGCCTGGG (SEQ ID NO:692); GAGCCTGGGA (SEQ ID NO:693);
AGCCTGGGAG (SEQ ID NO:694); GCCTGGGAGC (SEQ ID NO:695);
CCTGGGAGCT (SEQ ID NO:696); CTGGGAGCTC (SEQ ID NO:697);
TGGGAGCTCT (SEQ ID NO:698); GGGAGCTCTC (SEQ ID NO:699);
GGAGCTCTCT (SEQ ID NO:700); GAGCTCTCTG (SEQ ID NO:701);
AGCTCTCTGG (SEQ ID NO:702); GCTCTCTGGC (SEQ ID NO:703);
CTCTCTGGCT (SEQ ID NO:704); TCTCTGGCTA (SEQ ID NO:705);
CTCTGGCTAA (SEQ ID NO:706); TCTGGCTAAC (SEQ ID NO:707);
CTGGCTAACT (SEQ ID NO:708); TGGCTAACTA (SEQ ID NO:709);
GGCTAACTAG (SEQ ID NO:710); GCTAACTAGG (SEQ ID NO:711);
CTAACTAGGG (SEQ ID NO:712); TAACTAGGGA (SEQ ID NO:713);
AACTAGGGAA (SEQ ID NO:714); ACTAGGGAAC (SEQ ID NO:715);
CTAGGGAACC (SEQ ID NO:716); TAGGGAACCC (SEQ ID NO:717);
AGGGAACCCA (SEQ ID NO:718); GGGAAACCCAC (SEQ ID NO:719);
GGAACCCACT (SEQ ID NO:720); GAACCCACTG (SEQ ID NO:721);
AACCCACTGC (SEQ ID NO:722); ACCCACTGCT (SEQ ID NO:723);
CCCACTGCTT (SEQ ID NO:724); CCACTGCTTA (SEQ ID NO:725);
CACTGCTTAA (SEQ ID NO:726); ACTGCTTAAG (SEQ ID NO:727);
CTGCTTAAGC (SEQ ID NO:728); TGCTTAAGCC (SEQ ID NO:729);
GCTTAAGCCT (SEQ ID NO:730); CTTAAGCCTC (SEQ ID NO:731);
TTAAGCCTCA (SEQ ID NO:732); TAAGCCTCAA (SEQ ID NO:733);
AAGCCTCAAT (SEQ ID NO:734); AGCCTCAATA (SEQ ID NO:735);
GCCTCAATAA (SEQ ID NO:736); CCTCAATAAA (SEQ ID NO:737);
CTCAATAAAG (SEQ ID NO:738); TCAATAAAGC (SEQ ID NO:739);

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- 269 -

CAATAAAGCT (SEQ ID NO:740); AATAAAGCTT (SEQ ID NO:741);
 ATAAAGCTTG (SEQ ID NO:742); TAAAGCTTGC (SEQ ID NO:743);
 AAAGCTTGCC (SEQ ID NO:744); AAGCTTGCCT (SEQ ID NO:745);
 AGCTTGCCCTT (SEQ ID NO:746); GCTTGCCCTG (SEQ ID NO:747);
 CTTGCCTTGA (SEQ ID NO:748); TTGCCTTGAG (SEQ ID NO:749);
 TGCCTTGAGT (SEQ ID NO:750); GCCTTGAATG (SEQ ID NO:751);
 CCTTGAGTGC (SEQ ID NO:752); CTTGAGTGCT (SEQ ID NO:753);
 TTGAGTGCTT (SEQ ID NO:754); TGAGTGCTTC (SEQ ID NO:755);
 GAGTGCTTCA (SEQ ID NO:756); AGTGCTTCAA (SEQ ID NO:757);
 GTGCTTCAAG (SEQ ID NO:758); TGCTTCAAGT (SEQ ID NO:759);
 GCTTCAAGTA (SEQ ID NO:760); CTTCAAGTAG (SEQ ID NO:761);
 TTCAAGTAGT (SEQ ID NO:762); TCAAGTAGTG (SEQ ID NO:763);
 CAAGTAGTGT (SEQ ID NO:764); AAGTAGTGTG (SEQ ID NO:765);
 AGTAGTGTGT (SEQ ID NO:766); GTAGTGTGTG (SEQ ID NO:767);
 TAGTGTGTGC (SEQ ID NO:768); AGTGTGTGCC (SEQ ID NO:769);
 GTGTGTGCCC (SEQ ID NO:770); TGTGTGCCCC (SEQ ID NO:771);
 GTGTGCCCGT (SEQ ID NO:772); TGTGCCCGTC (SEQ ID NO:773);
 GTGCCCGTCT (SEQ ID NO:774); TGCCCGTCTG (SEQ ID NO:775);
 GCCCGTCTGT (SEQ ID NO:776); CCGTCTGTGT (SEQ ID NO:777);
 CCGTCTGTGT (SEQ ID NO:778); CGTGTGTGTG (SEQ ID NO:779);
 GTCGTGTGTG (SEQ ID NO:780); TGTGTGTGTG (SEQ ID NO:781);
 CTGTGTGTGT (SEQ ID NO:782); TGTGTGTGTA (SEQ ID NO:783);
 GTTGTGTGAC (SEQ ID NO:784); TTGTGTGACT (SEQ ID NO:785);
 TGTGTGACTC (SEQ ID NO:786); GTGTGACTCT (SEQ ID NO:787);
 TGTGTGACTC (SEQ ID NO:788); GTGTGACTCT (SEQ ID NO:789);
 TGTGACTCTG (SEQ ID NO:790); GTGACTCTGG (SEQ ID NO:791);
 TGA CTCTGGT (SEQ ID NO:792); GACTCTGGTA (SEQ ID NO:793);
 ACTCTGGTAA (SEQ ID NO:794); CTCTGGTAAC (SEQ ID NO:795);
 TCTGGTAACT (SEQ ID NO:796); CTGGTAACTA (SEQ ID NO:797);
 TGGTAACTAG (SEQ ID NO:798); GGTA ACTAGA (SEQ ID NO:799).

103. A method for determining the pathogenicity of an HIV-1 strain after said HIV-1 strain infects cells of an individual, said method comprising determining the presence of a deletion mutation in its genome of at least 10 nucleotides within the region from nucleotide 8787 to nucleotide 9709 using the nucleotide numbering of HIV-1_{NL43} wherein the presence of said deletion mutation is indicative of the presence of a non-pathogenic strain of HIV-1.

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- 270 -

104. A method according to claim 99 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(i)	8830-8862;
	(ii)	9009-9035;
	(iii)	9019-9029; and
	(iv)	9033-9049.

105. A method according to claim 99 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(v)	9281-9371;
	(vi)	9281-9362;
	(vii)	9105-9224; and
	(viii)	9271-9370.

106. A method according to claim 99 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(ix)	8882-8928;
	(x)	8850-9006;
	(xi)	8792-9041; and
	(xii)	9112-9204.

107. A method according to claim 99 wherein said non-pathogenic HIV-1 carries a deletion in its genome of at least 10 nucleotides from within a region selected from the list consisting of:

nucleotide	(xiii)	9105-9224;
	(xiv)	9389-9395; and
	(xv)	9281-9366.

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- 271 -

108. A method according to claim 99 wherein said deletion encompasses at least one of the following decanucleotides from the *nef* gene of HIV-1_{MLA3}:

ATGGGTGGCA (SEQ ID NO:2);	TGGGTGGCAA (SEQ ID NO:3);
GGGTGGCAAG (SEQ ID NO:4);	GGTGGCAAGT (SEQ ID NO:5);
GTGGCAAGTG (SEQ ID NO:6);	TGGCAAGTGG (SEQ ID NO:7);
GGCAAGTGGT (SEQ ID NO:8);	GCAAGTGGTC (SEQ ID NO:9);
CAAGTGGTCA (SEQ ID NO:10);	AAGTGGTCAA (SEQ ID NO:11);
AGTGGTCAAA (SEQ ID NO:12);	GTGGTCAAAA (SEQ ID NO:13);
TGGTCAAAA (SEQ ID NO:14);	GGTCAAAAAG (SEQ ID NO:15);
GTCAAAAAGT (SEQ ID NO:16);	TCAAAAAGTA (SEQ ID NO:17);
CAAAAAGTAG (SEQ ID NO:18);	AAAAAGTAGT (SEQ ID NO:19);
AAAAGTAGTG (SEQ ID NO:20);	AAAGTAGTGT (SEQ ID NO:21);
AAGTAGTGTG (SEQ ID NO:22);	AGTAGTGTGA (SEQ ID NO:23);
GTAGTGTGAT (SEQ ID NO:24);	TAGTGTGATT (SEQ ID NO:25);
AGTGTGATTG (SEQ ID NO:26);	GTGTGATTGG (SEQ ID NO:27);
TGTGATTGGA (SEQ ID NO:28);	GTGATTGGAT (SEQ ID NO:29);
TGATTGGATG (SEQ ID NO:30);	GATTGGATGG (SEQ ID NO:31);
ATTGGATGGC (SEQ ID NO:32);	TGGATGGGCC (SEQ ID NO:33);
TGGATGGCCT (SEQ ID NO:34);	GGATGGCCTG (SEQ ID NO:35);
GATGGCCTGC (SEQ ID NO:36);	ATGGCCTGCT (SEQ ID NO:37);
TGGCCTGCTG (SEQ ID NO:38);	GGCCTGCTGT (SEQ ID NO:39);
GCCTGCTGTA (SEQ ID NO:40);	CCTGCTGTAA (SEQ ID NO:41);
CTGCTGTAA (SEQ ID NO:42);	TGCTGTAAAG (SEQ ID NO:43);
GCTGTAAAGG (SEQ ID NO:44);	CTGTAAAGGA (SEQ ID NO:45);
TGTAAAGGAA (SEQ ID NO:46);	GTAAAGGAAA (SEQ ID NO:47);
TAAGGGAAG (SEQ ID NO:48);	AAGGGAAGAA (SEQ ID NO:49);
AGGGAAGAA (SEQ ID NO:50);	GGAAGGAAT (SEQ ID NO:51);
GGAAAGAATG (SEQ ID NO:52);	GAAAGAATGA (SEQ ID NO:53);
AAAGAATGAG (SEQ ID NO:54);	AAGAATGAGA (SEQ ID NO:55);
AGAATGAGAC (SEQ ID NO:56);	GAATGAGACG (SEQ ID NO:57);
AATGAGACGA (SEQ ID NO:58);	ATGAGACGAG (SEQ ID NO:59);
TGAGACGAGC (SEQ ID NO:60);	GAGACGAGCT (SEQ ID NO:61);
AGACGAGCTG (SEQ ID NO:62);	GACGAGCTGA (SEQ ID NO:63);
ACGAGCTGAG (SEQ ID NO:64);	CGAGCTGAGC (SEQ ID NO:65);
GAGCTGAGCC (SEQ ID NO:66);	AGCTGAGCCA (SEQ ID NO:67);
GCTGAGCCAG (SEQ ID NO:68);	CTGAGCCAGC (SEQ ID NO:69);

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- 272 -

TGAGCCAGCA (SEQ ID NO:70);	GAGCCAGCAG (SEQ ID NO:71);
AGCCAGCAGC (SEQ ID NO:72);	GCCAGCAGCA (SEQ ID NO:73);
CCAGCAGCAG (SEQ ID NO:74);	CAGCAGCAGA (SEQ ID NO:75);
AGCAGCAGAT (SEQ ID NO:76);	GCAGCAGATG (SEQ ID NO:77);
CAGCAGATGG (SEQ ID NO:78);	AGCAGATGGG (SEQ ID NO:79);
GCAGATGGGG (SEQ ID NO:80);	CAGATGGGGT (SEQ ID NO:81);
AGATGGGGTG (SEQ ID NO:82);	GATGGGGTGG (SEQ ID NO:83);
ATGGGGTGGG (SEQ ID NO:84);	TGGGGTGGGA (SEQ ID NO:85);
GGGGTGGGAG (SEQ ID NO:86);	GGGTGGGAGC (SEQ ID NO:87);
GGTGGGAGCA (SEQ ID NO:88);	GTGGGAGCAG (SEQ ID NO:89);
TGGGAGCAGT (SEQ ID NO:90);	GGGAGCAGTA (SEQ ID NO:91);
GGAGCAGTAT (SEQ ID NO:92);	GAGCAGTATC (SEQ ID NO:93);
AGCAGTATCT (SEQ ID NO:94);	GCAGTATCTC (SEQ ID NO:95);
CAGTATCTCG (SEQ ID NO:96);	AGTATCTCGA (SEQ ID NO:97);
GTATCTCGAG (SEQ ID NO:98);	TATCTCGAGA (SEQ ID NO:99);
ATCTCGAGAC (SEQ ID NO:100);	TCTCGAGACC (SEQ ID NO:101);
CTCGAGACCT (SEQ ID NO:102);	TOGAGACCTA (SEQ ID NO:103);
CGAGACCTAG (SEQ ID NO:104);	GAGACCTAGA (SEQ ID NO:105);
AGACCTAGAA (SEQ ID NO:106);	GAGCTAGAAA (SEQ ID NO:107);
ACCTAGAAAA (SEQ ID NO:108);	CCTAGAAAAA (SEQ ID NO:109);
CTAGAAAAAC (SEQ ID NO:110);	TAGAAAAACA (SEQ ID NO:111);
AGAAAAACAT (SEQ ID NO:112);	GAAAAACATG (SEQ ID NO:113);
AAAAACATGG (SEQ ID NO:114);	AAAACATGGA (SEQ ID NO:115);
AAACATGGAG (SEQ ID NO:116);	AACATGGAGC (SEQ ID NO:117);
ACATGGAGCA (SEQ ID NO:118);	CATGGAGCAA (SEQ ID NO:119);
ATGGAGCAAT (SEQ ID NO:120);	TGGAGCAATC (SEQ ID NO:121);
GGAGCAATCA (SEQ ID NO:122);	GAGCAATCAC (SEQ ID NO:123);
AGCAATCACA (SEQ ID NO:124);	GCAATCACAA (SEQ ID NO:125);
CAATCACAAG (SEQ ID NO:126);	AATCACAAGT (SEQ ID NO:127);
ATCACAAGTA (SEQ ID NO:128);	TCACAAGTAG (SEQ ID NO:129);
CACAAGTAGC (SEQ ID NO:130);	ACAAGTAGCA (SEQ ID NO:131);
CAAGTAGCAA (SEQ ID NO:132);	AAGTAGCAAT (SEQ ID NO:133);
AGTAGCAATA (SEQ ID NO:134);	GTAGCAATAC (SEQ ID NO:135);
TAGCAATACA (SEQ ID NO:136);	AGCAATACAG (SEQ ID NO:137);
GCAATACAGC (SEQ ID NO:138);	CAATACAGCA (SEQ ID NO:139);
AATACAGCAG (SEQ ID NO:140);	ATACAGCAGC (SEQ ID NO:141);
TACAGCAGCT (SEQ ID NO:142);	ACAGCAGCTA (SEQ ID NO:143);
CAGCAGCTAA (SEQ ID NO:144);	AGCAGCTAAC (SEQ ID NO:145);

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- 273 -

GCAGCTAACA (SEQ ID NO:146); CAGCTAACAA (SEQ ID NO:147);
AGCTAACAAAT (SEQ ID NO:148); GCTAACAAATG (SEQ ID NO:149);
CTAACAAATGC (SEQ ID NO:150); TAACAAATGCT (SEQ ID NO:151);
AACAAATGCTG (SEQ ID NO:152); ACAATGCTGC (SEQ ID NO:153);
CAATGCTGCT (SEQ ID NO:154); AATGCTGCTT (SEQ ID NO:155);
ATGCTGCTTG (SEQ ID NO:156); TGCTGCTTGT (SEQ ID NO:157);
GCTGCTTGTG (SEQ ID NO:158); CTGCTTGTGC (SEQ ID NO:159);
TGCTTGTGCC (SEQ ID NO:160); GCTTGTGCCT (SEQ ID NO:161);
CTTGTGCCCTG (SEQ ID NO:162); TTGTGCCCTGG (SEQ ID NO:163);
TGTGCCCTGGC (SEQ ID NO:164); GTGCCCTGGCT (SEQ ID NO:165);
TGCCTGGCTA (SEQ ID NO:166); GGCTGGCTAG (SEQ ID NO:167);
CCTGGCTAGA (SEQ ID NO:168); CTGGCTAGAA (SEQ ID NO:169);
TGGCTAGAAG (SEQ ID NO:170); GGCTAGAAGC (SEQ ID NO:171);
GCTAGAAGCA (SEQ ID NO:172); CTAGAAGCAC (SEQ ID NO:173);
TAGAAGCACA (SEQ ID NO:174); AGAAGCACAA (SEQ ID NO:175);
GAAGCACAAAG (SEQ ID NO:176); AAGCACAAAG (SEQ ID NO:177);
AGCACAAAGAG (SEQ ID NO:178); GCACAAAGAGG (SEQ ID NO:179);
CACAAAGAGGA (SEQ ID NO:180); ACAAGAGGAG (SEQ ID NO:181);
CAAGAGGAGG (SEQ ID NO:182); AAGAGGAGGA (SEQ ID NO:183);
AGAGGAGGAA (SEQ ID NO:184); GAGGAGGAAG (SEQ ID NO:185);
AGGAGGAAGA (SEQ ID NO:186); GGAGGAAGAG (SEQ ID NO:187);
GAGGAAGAGG (SEQ ID NO:188); AGGAAGAGGT (SEQ ID NO:189);
GGAAGAGGTG (SEQ ID NO:190); GAAGAGGTGG (SEQ ID NO:191);
AAGAGGTGGG (SEQ ID NO:192); AGAGGTGGGT (SEQ ID NO:193);
GAGGTGGGTT (SEQ ID NO:194); AGGTGGGTTT (SEQ ID NO:195);
GGTGGGTTTT (SEQ ID NO:196); GTGGGTTTTT (SEQ ID NO:197);
TGGGTTTTTCC (SEQ ID NO:198); GGGTTTTTCCA (SEQ ID NO:199);
GGTTTTTCCAG (SEQ ID NO:200); GTTTTTCCAGT (SEQ ID NO:201);
TTTTCCAGTC (SEQ ID NO:202); TTTCAGTCA (SEQ ID NO:203);
TTCCAGTCAC (SEQ ID NO:204); TCCAGTCACA (SEQ ID NO:205);
CCAGTCACAC (SEQ ID NO:206); CAGTCACACC (SEQ ID NO:207);
AGTCACACCT (SEQ ID NO:208); GTCACACCTC (SEQ ID NO:209);
TCACACCTCA (SEQ ID NO:210); CACACCTCAG (SEQ ID NO:211);
ACACCTCAGG (SEQ ID NO:212); CACCTCAGGT (SEQ ID NO:213);
ACCTCAGGTA (SEQ ID NO:214); CCTCAGGTAC (SEQ ID NO:215);
CTCAGGTACC (SEQ ID NO:216); TCAGGTACCT (SEQ ID NO:217);
CAGGTACCTT (SEQ ID NO:218); AGGTACCTTT (SEQ ID NO:219);
GGTACCTTTA (SEQ ID NO:220); GTACCTTTAA (SEQ ID NO:221);

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- 274 -

TACCTTTAAG (SEQ ID NO:222);	ACCTTTAAGA (SEQ ID NO:223);
CCTTTAAGAC (SEQ ID NO:224);	CTTTAAGACC (SEQ ID NO:225);
TTTAAGACCA (SEQ ID NO:226);	TTAAGACCAA (SEQ ID NO:227);
TAAGACCAAT (SEQ ID NO:228);	AAGACCAATG (SEQ ID NO:229);
AGACCAATGA (SEQ ID NO:230);	GACCAATGAC (SEQ ID NO:231);
ACCAATGACT (SEQ ID NO:232);	CCAATGACTT (SEQ ID NO:233);
CAATGACTTA (SEQ ID NO:234);	AATGACTTAC (SEQ ID NO:235);
ATGACTTACA (SEQ ID NO:236);	TGACTTACAA (SEQ ID NO:237);
GACTTACAAG (SEQ ID NO:238);	ACTTACAAGG (SEQ ID NO:239);
CTTACAAGGC (SEQ ID NO:240);	TTACAAGGCA (SEQ ID NO:241);
TACAAGGCAG (SEQ ID NO:242);	ACAAGGCAGC (SEQ ID NO:243);
CAAGGCAGCT (SEQ ID NO:244);	AAGGCAGCTG (SEQ ID NO:245);
AGGCAGCTGT (SEQ ID NO:246);	GGCAGCTGTA (SEQ ID NO:247);
GCAGCTGTAG (SEQ ID NO:248);	CAGCTGTAGA (SEQ ID NO:249);
AGCTGTAGAT (SEQ ID NO:250);	GCTGTAGATC (SEQ ID NO:251);
CTGTAGATCT (SEQ ID NO:252);	TGTAGATCTT (SEQ ID NO:253);
GTAGATCTTA (SEQ ID NO:254);	TAGATCTTAG (SEQ ID NO:255);
AGATCTTAGC (SEQ ID NO:256);	GATCTTAGCC (SEQ ID NO:257);
ATCTTAGCCA (SEQ ID NO:258);	TCTTAGCCAC (SEQ ID NO:259);
CTTAGCCACT (SEQ ID NO:260);	TTAGCCACTT (SEQ ID NO:261);
TAGCCACTTT (SEQ ID NO:262);	AGCCACTTTT (SEQ ID NO:263);
GCCACTTTTT (SEQ ID NO:264);	CCACTTTTTA (SEQ ID NO:265);
CACTTTTTAA (SEQ ID NO:266);	ACTTTTTAAA (SEQ ID NO:267);
CTTTTTAAAA (SEQ ID NO:268);	TTTTTAAAG (SEQ ID NO:269);
TTTTAAAGA (SEQ ID NO:270);	TTTAAAGAA (SEQ ID NO:271);
TTAAAGAAA (SEQ ID NO:272);	TAAAGAAAA (SEQ ID NO:273);
AAAAGAAAAG (SEQ ID NO:274);	AAAGAAAAGG (SEQ ID NO:275);
AAGAAAAGGG (SEQ ID NO:276);	AGAAAAGGGG (SEQ ID NO:277);
GAAAAGGGGG (SEQ ID NO:278);	AAAAGGGGGG (SEQ ID NO:279);
AAAGGGGGGA (SEQ ID NO:280);	AAGGGGGGAC (SEQ ID NO:281);
AGGGGGGACT (SEQ ID NO:282);	GGGGGGGACTG (SEQ ID NO:283);
GGGGGACTGG (SEQ ID NO:284);	GGGGACTGGA (SEQ ID NO:285);
GGGACTGGAA (SEQ ID NO:286);	GGACTGGAAG (SEQ ID NO:287);
GACTGGAAGG (SEQ ID NO:288);	ACTGGAAGGG (SEQ ID NO:289);
CTGGAAGGGC (SEQ ID NO:290);	TGGAAGGGCT (SEQ ID NO:291);
GGAAGGGCTA (SEQ ID NO:292);	GAAGGGCTAA (SEQ ID NO:293);
AAGGGCTAAT (SEQ ID NO:294);	AGGGCTAATT (SEQ ID NO:295);
GGGCTAATTC (SEQ ID NO:296);	GGCTAATTCA (SEQ ID NO:297);

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- 275 -

GCTAATTCAC (SEQ ID NO:298); CTAATTCACT (SEQ ID NO:299);
TAATTCACTC (SEQ ID NO:300); AATTCACTCC (SEQ ID NO:301);
ATTCACTCCC (SEQ ID NO:302); TTCACTCCCA (SEQ ID NO:303);
TCACTCCCAA (SEQ ID NO:304); CACTCCCAA (SEQ ID NO:305);
ACTCCCAAAG (SEQ ID NO:306); CTCOCNAAGA (SEQ ID NO:307);
TCCCAAAGAA (SEQ ID NO:308); CCCAAAGAAG (SEQ ID NO:309);
CCAAAGAAGA (SEQ ID NO:310); CAAAGAAGAC (SEQ ID NO:311);
AAAGAAGACA (SEQ ID NO:312); AAGAAGACAA (SEQ ID NO:313);
AGAAGACAAG (SEQ ID NO:314); GAAGACAAGA (SEQ ID NO:315);
AAGACAAGAT (SEQ ID NO:316); AGACAAGATA (SEQ ID NO:317);
GACAAGATAT (SEQ ID NO:318); ACAAGATATC (SEQ ID NO:319);
CAAGATATCC (SEQ ID NO:320); AAGATATCCT (SEQ ID NO:321);
AGATATCCTT (SEQ ID NO:322); GATATCCTTG (SEQ ID NO:323);
ATATCCTTGA (SEQ ID NO:324); TATCCTTGAT (SEQ ID NO:325);
ATCCTTGATC (SEQ ID NO:326); TCCTTGATCT (SEQ ID NO:327);
CCTTGATCTG (SEQ ID NO:328); CTTGATCTGT (SEQ ID NO:329);
TTGATCTGTG (SEQ ID NO:330); TGATCTGTGG (SEQ ID NO:331);
GATCTGTGGA (SEQ ID NO:332); ATCTGTGGAT (SEQ ID NO:333);
TCTGTGGATC (SEQ ID NO:334); CTGTGGATCT (SEQ ID NO:335);
TGTGGATCTA (SEQ ID NO:336); GTGGATCTAC (SEQ ID NO:337);
TGGATCTACC (SEQ ID NO:338); GGATCTACCA (SEQ ID NO:339);
GATCTACCAC (SEQ ID NO:340); ATGTACCACA (SEQ ID NO:341);
TCTACCACAC (SEQ ID NO:342); CTAGCACACA (SEQ ID NO:343);
TACCACACAC (SEQ ID NO:344); ACCACACACA (SEQ ID NO:345);
CCACACACAA (SEQ ID NO:346); CACACACAAG (SEQ ID NO:347);
ACACACAAGG (SEQ ID NO:348); CACACAAGGC (SEQ ID NO:349);
ACACAAGGCT (SEQ ID NO:350); CACAAGGCTA (SEQ ID NO:351);
ACAAGGCTAC (SEQ ID NO:352); CAAGGCTACT (SEQ ID NO:353);
AAGGCTACTT (SEQ ID NO:354); AGGCTACTTC (SEQ ID NO:355);
GGCTACTTCC (SEQ ID NO:356); GCTACTTCCC (SEQ ID NO:357);
CTACTTCCCT (SEQ ID NO:358); TACTTCCCTG (SEQ ID NO:359);
ACTTCCCTGA (SEQ ID NO:360); CTTCCCTGAT (SEQ ID NO:361);
TTCCCTGATT (SEQ ID NO:362); TCCTTGATTG (SEQ ID NO:363);
CCCTGATTGG (SEQ ID NO:364); CCTGATTGGC (SEQ ID NO:365);
CTGATTGGCA (SEQ ID NO:366); TGATTGGCAG (SEQ ID NO:367);
GATTGGCAGA (SEQ ID NO:368); ATTGGCAGAA (SEQ ID NO:369);
TTGGCAGAAC (SEQ ID NO:370); TGGCAGAACT (SEQ ID NO:371);
GGCAGAACTA (SEQ ID NO:372); GCAGAACTAC (SEQ ID NO:373);

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- 276 -

CAGAACTACA (SEQ ID NO:374); AGAACTACAC (SEQ ID NO:375);
GAACTACACA (SEQ ID NO:376); AACTACACAC (SEQ ID NO:377);
ACTACACACC (SEQ ID NO:378); CTACACACCA (SEQ ID NO:379);
TACACACCAG (SEQ ID NO:380); ACACACCAGG (SEQ ID NO:381);
CACACCAGGG (SEQ ID NO:382); ACACCAGGGC (SEQ ID NO:383);
CACCAGGGCC (SEQ ID NO:384); ACCAGGGCCA (SEQ ID NO:385);
CCAGGGCCAG (SEQ ID NO:386); CAGGGCCAGG (SEQ ID NO:387);
AGGGCCAGGG (SEQ ID NO:388); GGGCCAGGGG (SEQ ID NO:389);
GGCCAGGGGT (SEQ ID NO:390); GCCAGGGGTC (SEQ ID NO:391);
CCAGGGGTCA (SEQ ID NO:392); CAGGGGTCAG (SEQ ID NO:393);
AGGGGTCAGA (SEQ ID NO:394); GGGGTCAGAT (SEQ ID NO:395);
GGGTCAGATA (SEQ ID NO:396); GGTCAGATAT (SEQ ID NO:397);
GTCAGATATC (SEQ ID NO:398); TCGATATATC (SEQ ID NO:399);
CAGATATCCA (SEQ ID NO:400); AGATATCCAC (SEQ ID NO:401);
GATATCCACT (SEQ ID NO:402); ATATCCACTG (SEQ ID NO:403);
TATCCACTGA (SEQ ID NO:404); ATGCACTGAC (SEQ ID NO:405);
TCCACTGACC (SEQ ID NO:406); CCACTGACCT (SEQ ID NO:407);
CACTGACCTT (SEQ ID NO:408); ACTGACCTTT (SEQ ID NO:409);
CTGACCTTTG (SEQ ID NO:410); TGACCTTTGG (SEQ ID NO:411);
GACCTTTGGA (SEQ ID NO:412); ACGTTTGGAT (SEQ ID NO:413);
CCTTTGGATG (SEQ ID NO:414); CTTTGGATGG (SEQ ID NO:415);
TTTGGATGGT (SEQ ID NO:416); TTGGATGGTG (SEQ ID NO:417);
TGGATGGTGC (SEQ ID NO:418); GGATGGTGCT (SEQ ID NO:419);
GATGGTGCTA (SEQ ID NO:420); ATGGTGCTAC (SEQ ID NO:421);
TGGTGCTACA (SEQ ID NO:422); GGTGCTACAA (SEQ ID NO:423);
GTGCTACAAG (SEQ ID NO:424); TGCTACAAGC (SEQ ID NO:425);
GCTACAAGCT (SEQ ID NO:426); CTACAAGCTA (SEQ ID NO:427);
TACAAGCTAG (SEQ ID NO:428); ACAAGCTAGT (SEQ ID NO:429);
CAAGCTAGTA (SEQ ID NO:430); AAGCTAGTAC (SEQ ID NO:431);
AGCTAGTACC (SEQ ID NO:432); GCTAGTACCA (SEQ ID NO:433);
CTAGTACCAG (SEQ ID NO:434); TAGTACCAGT (SEQ ID NO:435);
AGTACCAGTT (SEQ ID NO:436); GTACCAGTTG (SEQ ID NO:437);
TACCAGTTGA (SEQ ID NO:438); ACCAGTTGAG (SEQ ID NO:439);
CCAGTTGAGC (SEQ ID NO:440); CAGTTGAGCC (SEQ ID NO:441);
AGTTGAGCCA (SEQ ID NO:442); GTTGAGCCAG (SEQ ID NO:443);
TTGAGCCAGA (SEQ ID NO:444); TGAGCCAGAT (SEQ ID NO:445);
GAGCCAGATA (SEQ ID NO:446); AGCCAGATAA (SEQ ID NO:447);
GCCAGATAAG (SEQ ID NO:448); CCAGATAAGG (SEQ ID NO:449);

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- 277 -

CAGATAAGGT (SEQ ID NO:450); AGATAAGGTA (SEQ ID NO:451);
GATAAGGTAG (SEQ ID NO:452); ATAAGGTAGA (SEQ ID NO:453);
TAAGGTAGAA (SEQ ID NO:454); AAGGTAGAAG (SEQ ID NO:455);
AGGTAGAAGA (SEQ ID NO:456); GGTAGAAGAG (SEQ ID NO:457);
GTAGAAGAGG (SEQ ID NO:458); TAGAAGAGGC (SEQ ID NO:459);
AGAAGAGGCC (SEQ ID NO:460); GAAGAGGCCA (SEQ ID NO:461);
AAGAGGCCAA (SEQ ID NO:462); AGAGGCCAAT (SEQ ID NO:463);
GAGGCCAATA (SEQ ID NO:464); AGGCCAATAA (SEQ ID NO:465);
GGCCAATAAA (SEQ ID NO:466); GCCAATAAAG (SEQ ID NO:467);
CCAATAAAGG (SEQ ID NO:468); CAATAAAGGA (SEQ ID NO:469);
AATAAAGGAG (SEQ ID NO:470); ATAAAGGAGA (SEQ ID NO:471);
TAAAGGAGAG (SEQ ID NO:472); AAAGGAGAGA (SEQ ID NO:473);
AAGGAGAGAA (SEQ ID NO:474); AGGAGAGAAC (SEQ ID NO:475);
GGAGAGAACAA (SEQ ID NO:476); GAGAGAACAC (SEQ ID NO:477);
AGAGAACACC (SEQ ID NO:478); GAGAACACCA (SEQ ID NO:479);
AGAACACCAG (SEQ ID NO:480); GAACACCAGC (SEQ ID NO:481);
AACACCAGCT (SEQ ID NO:482); ACACCAGCTT (SEQ ID NO:483);
CACCAGCTTG (SEQ ID NO:484); ACCAGCTTGT (SEQ ID NO:485);
CCAGCTTGTT (SEQ ID NO:486); CAGCTTGTTA (SEQ ID NO:487);
AGCTTGTTAC (SEQ ID NO:488); GCTTGTTACA (SEQ ID NO:489);
CTTGTTACAC (SEQ ID NO:490); TTGTTACACC (SEQ ID NO:491);
TGTTACACCC (SEQ ID NO:492); GTTACACCCT (SEQ ID NO:493);
TTACACCCCTG (SEQ ID NO:494); TACACCCCTGT (SEQ ID NO:495);
ACACCCCTGTG (SEQ ID NO:496); CACCCCTGTGA (SEQ ID NO:497);
ACCCTGTGAG (SEQ ID NO:498); CCTGTGAGC (SEQ ID NO:499);
CCTGTGAGCC (SEQ ID NO:500); CTGTGAGCCT (SEQ ID NO:501);
TGTGAGCCTG (SEQ ID NO:502); GTGAGCCTGC (SEQ ID NO:503);
TGAGCCTGCA (SEQ ID NO:504); GAGCCTGCAT (SEQ ID NO:505);
AGCCTGCATG (SEQ ID NO:506); GCCTGCATGG (SEQ ID NO:507);
CCTGCATGGA (SEQ ID NO:508); CTGCATGGAA (SEQ ID NO:509);
TGCATGGAAT (SEQ ID NO:510); GCATGGAATG (SEQ ID NO:511);
CATGGAATGG (SEQ ID NO:512); ATGGAATGGA (SEQ ID NO:513);
TGGAATGGAT (SEQ ID NO:514); GGAATGGATG (SEQ ID NO:515);
GAATGGATGA (SEQ ID NO:516); AATGGATGAC (SEQ ID NO:517);
ATGGATGACC (SEQ ID NO:518); TGGATGACCC (SEQ ID NO:519);
GGATGACCCT (SEQ ID NO:520); GATGACCCTG (SEQ ID NO:521);
ATGACCCTGA (SEQ ID NO:522); TGACCCTGAG (SEQ ID NO:523);
GACCCTGAGA (SEQ ID NO:524); ACCCTGAGAG (SEQ ID NO:525);

00146783-090360-EBZSH160

- 278 -

CCCTGAGAGA (SEQ ID NO:526);	CCTGAGAGAG (SEQ ID NO:527);
CTGAGAGAGA (SEQ ID NO:528);	TGAGAGAGAA (SEQ ID NO:529);
GAGAGAGAAG (SEQ ID NO:530);	AGAGAGAAAGT (SEQ ID NO:531);
GAGAGAAAGTG (SEQ ID NO:532);	AGAGAAAGTGT (SEQ ID NO:533);
GAGAAGTGTT (SEQ ID NO:534);	AGAAGTGTTA (SEQ ID NO:535);
GAAGTGTTAG (SEQ ID NO:536);	AAGTGTTAGA (SEQ ID NO:537);
AGTGTTAGAG (SEQ ID NO:538);	GTGTTAGAGT (SEQ ID NO:539);
TGTTAGAGTG (SEQ ID NO:540);	GTTAGAGTGG (SEQ ID NO:541);
TTAGAGTGGA (SEQ ID NO:542);	TAGAGTGGAG (SEQ ID NO:543);
AGAGTGGAGG (SEQ ID NO:544);	GAGTGGAGGT (SEQ ID NO:545);
AGTGGAGGTT (SEQ ID NO:546);	GTTGGAGGTTT (SEQ ID NO:547);
TGGAGGTTTG (SEQ ID NO:548);	GGGGTTTGGA (SEQ ID NO:549);
GAGGTTTGAC (SEQ ID NO:550);	AGGTTTGACA (SEQ ID NO:551);
GGTTTGACAG (SEQ ID NO:552);	GTTTGACAGC (SEQ ID NO:553);
TTTGACAGCC (SEQ ID NO:554);	TTGACAGCCG (SEQ ID NO:555);
TGACAGCCGC (SEQ ID NO:556);	GAGAGCCGCC (SEQ ID NO:557);
ACAGCCGCCT (SEQ ID NO:558);	CAGCCGCCTA (SEQ ID NO:559);
AGCCGCCTAG (SEQ ID NO:560);	GGCCGCCTAGC (SEQ ID NO:561);
CCGCCTAGCA (SEQ ID NO:562);	CGCCTAGCAT (SEQ ID NO:563);
GCCTAGCATT (SEQ ID NO:564);	CCTAGCATTT (SEQ ID NO:565);
CTAGCATTTT (SEQ ID NO:566);	TAGCATTTCA (SEQ ID NO:567);
AGCATTTTCA (SEQ ID NO:568);	GCATTTTCATC (SEQ ID NO:569);
CATTTTCATCA (SEQ ID NO:570);	ATTTTCATCAC (SEQ ID NO:571);
TTTCATCACG (SEQ ID NO:572);	TTTCATCACGT (SEQ ID NO:573);
TCATCACGTG (SEQ ID NO:574);	CATCACGTGG (SEQ ID NO:575);
ATCACGTGGC (SEQ ID NO:576);	TCAAGTGGCC (SEQ ID NO:577);
CACGTGGCCC (SEQ ID NO:578);	AGGTGGCCCG (SEQ ID NO:579);
CGTGGCCCGA (SEQ ID NO:580);	GTTGGCCCGAG (SEQ ID NO:581);
TGGCCCGAGA (SEQ ID NO:582);	GGCCCGAGAG (SEQ ID NO:583);
GCCCGAGAGC (SEQ ID NO:584);	CCCGAGAGCT (SEQ ID NO:585);
CCGAGAGCTG (SEQ ID NO:586);	CGAGAGCTGC (SEQ ID NO:587);
GAGAGCTGCA (SEQ ID NO:588);	AGAGCTGCAT (SEQ ID NO:589);
GAGCTGCATC (SEQ ID NO:590);	AGCTGCATCC (SEQ ID NO:591);
GCTGCATCCG (SEQ ID NO:592);	CTGCATCCGG (SEQ ID NO:593);
TGCATCCGGA (SEQ ID NO:594);	GCATCCGGAG (SEQ ID NO:595);
CATCCGGAGT (SEQ ID NO:596);	ATCCGGAGTA (SEQ ID NO:597);
TCCGGAGTAC (SEQ ID NO:598);	CCGGAGTACT (SEQ ID NO:599);
CGGAGTACTT (SEQ ID NO:600);	GGAGTACTTC (SEQ ID NO:601);

- 279 -

109. A method according to claim 103 wherein said deletion encompasses at least one of the following decanucleotides from *nef* gene of HIV-1_{NL43}:

110. A method according to claim 103 wherein said deletion encompasses at least one of the following decanucleotides from the LTR region of HIV-1_{NI43}:

GCTTTTGGCC	(SEQ ID NO:652);	CTTTTGCCT	(SEQ ID NO:653);
TTTTGCCTG	(SEQ ID NO:654);	TTTGCCTGT	(SEQ ID NO:655);
TTGCCTGTA	(SEQ ID NO:656);	TGCTGTAC	(SEQ ID NO:657);
TGCTGTACT	(SEQ ID NO:658);	GCCTGTACTG	(SEQ ID NO:659);
CCTGTACTGG	(SEQ ID NO:660);	CTGTACTGGG	(SEQ ID NO:661);

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- 280 -

TGTACTGGGT	(SEQ ID NO:662);	GTACTGGGTC	(SEQ ID NO:663);
TACTGGGTCT	(SEQ ID NO:664);	ACTGGGTCTC	(SEQ ID NO:665);
CTGGGTCTCT	(SEQ ID NO:666);	TGGGTCTCTC	(SEQ ID NO:667);
GGGTCTCTCT	(SEQ ID NO:668);	GGTCTCTCTG	(SEQ ID NO:669);
GTCTCTCTGG	(SEQ ID NO:670);	TCTCTCTGGT	(SEQ ID NO:671);
CTCTCTGGTT	(SEQ ID NO:672);	TCTCTGGTTA	(SEQ ID NO:673);
CTCTGGTTAG	(SEQ ID NO:674);	TCTCTGGTTA	(SEQ ID NO:675);
CTGGTTAGAC	(SEQ ID NO:676);	TGGTTAGACC	(SEQ ID NO:677);
GGTTAGACCA	(SEQ ID NO:678);	GTTAGACCAG	(SEQ ID NO:679);
TTAGACCAGA	(SEQ ID NO:680);	TAGACCAGAT	(SEQ ID NO:681);
AGACCAGATC	(SEQ ID NO:682);	GACCAGATCT	(SEQ ID NO:683);
ACCAGATCTG	(SEQ ID NO:684);	CCAGATCTGA	(SEQ ID NO:685);
CAGATCTGAG	(SEQ ID NO:686);	AGATCTGAGC	(SEQ ID NO:687);
GATCTGAGCC	(SEQ ID NO:688);	ATCTGAGCCT	(SEQ ID NO:689);
TCTGAGCCTG	(SEQ ID NO:690);	CTGAGCCTGG	(SEQ ID NO:691);
TGAGCCTGGG	(SEQ ID NO:692);	GAGCCTGGGA	(SEQ ID NO:693);
AGCCTGGGAG	(SEQ ID NO:694);	GCCTGGGAGC	(SEQ ID NO:695);
CCTGGGAGCT	(SEQ ID NO:696);	CTGGGAGCTC	(SEQ ID NO:697);
TGGGAGCTCT	(SEQ ID NO:698);	GGGAGCTCTC	(SEQ ID NO:699);
GGAGCTCTCT	(SEQ ID NO:700);	GAGCTCTCTG	(SEQ ID NO:701);
AGCTCTCTGG	(SEQ ID NO:702);	GCTCTCTGGC	(SEQ ID NO:703);
CTCTCTGGCT	(SEQ ID NO:704);	TCTCTGGCTA	(SEQ ID NO:705);
CTCTGGCTAA	(SEQ ID NO:706);	TCTGGCTAAC	(SEQ ID NO:707);
CTGGCTAACT	(SEQ ID NO:708);	TGGCTAACTA	(SEQ ID NO:709);
GGCTAACTAG	(SEQ ID NO:710);	GCTAACTAGG	(SEQ ID NO:711);
CTAACTAGGG	(SEQ ID NO:712);	TAACTAGGGA	(SEQ ID NO:713);
AACTAGGGAA	(SEQ ID NO:714);	ACTAGGGAAC	(SEQ ID NO:715);
CTAGGGAAACC	(SEQ ID NO:716);	TAGGGAAACC	(SEQ ID NO:717);
AGGGAAACCA	(SEQ ID NO:718);	GGGAACCCAC	(SEQ ID NO:719);
GGAACCCACT	(SEQ ID NO:720);	GAACCCACTG	(SEQ ID NO:721);
AACCCACTGC	(SEQ ID NO:722);	AGCCACTGCT	(SEQ ID NO:723);
CCCACTGCTT	(SEQ ID NO:724);	CCACTGCTTA	(SEQ ID NO:725);
CACTGCTTAA	(SEQ ID NO:726);	ACTGCTTAAG	(SEQ ID NO:727);
CTGCTTAAGC	(SEQ ID NO:728);	TGCTTAAGCC	(SEQ ID NO:729);
GCTTAAGCCT	(SEQ ID NO:730);	CTTAAGCCTC	(SEQ ID NO:731);
TTAAGCCTCA	(SEQ ID NO:732);	TAAGCCTCAA	(SEQ ID NO:733);
AAGCCTCAAT	(SEQ ID NO:734);	AGCCTCAATA	(SEQ ID NO:735);
GCCTCAATAA	(SEQ ID NO:736);	CCTCAATAAA	(SEQ ID NO:737);

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THE
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PART I.
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CTCAATAAAG	(SEQ ID NO:738);	TCAATAAAGC	(SEQ ID NO:739);
CAATAAAGCT	(SEQ ID NO:740);	AATAAAGCTT	(SEQ ID NO:741);
ATAAAGCTTG	(SEQ ID NO:742);	TAAAGCTTGC	(SEQ ID NO:743);
AAAGCTTGCC	(SEQ ID NO:744);	AAGCTTGCCT	(SEQ ID NO:745);
AGCTTGCCCT	(SEQ ID NO:746);	GCTTGCCCTG	(SEQ ID NO:747);
CTTGCCCTGA	(SEQ ID NO:748);	TTGCCCTGAG	(SEQ ID NO:749);
TGCCCTGAGT	(SEQ ID NO:750);	GCCTTGAGTG	(SEQ ID NO:751);
CCTTGAGTGC	(SEQ ID NO:752);	CTTGAGTGCT	(SEQ ID NO:753);
TTGAGTGCTT	(SEQ ID NO:754);	TGAGTGCTTC	(SEQ ID NO:755);
GAGTGCTTCA	(SEQ ID NO:756);	AGTGCTTCAA	(SEQ ID NO:757);
GTGCTTCAAG	(SEQ ID NO:758);	TGCTTCAAGT	(SEQ ID NO:759);
GCTTCAAGTA	(SEQ ID NO:760);	CTTCAAGTAG	(SEQ ID NO:761);
TTCAAGTAGT	(SEQ ID NO:762);	TCAAGTAGTG	(SEQ ID NO:763);
CAAGTAGTGT	(SEQ ID NO:764);	AAGTAGTGTG	(SEQ ID NO:765);
AGTAGTGTGT	(SEQ ID NO:766);	GTAGTGTGTG	(SEQ ID NO:767);
TAGTGTGTGC	(SEQ ID NO:768);	AGTGTGTGCC	(SEQ ID NO:769);
GTGTGTGCCC	(SEQ ID NO:770);	TGTGTGCCCC	(SEQ ID NO:771);
GTGTGCCCCG	(SEQ ID NO:772);	TGTGCCCCGC	(SEQ ID NO:773);
GTGCCCCGTCT	(SEQ ID NO:774);	TGCCCCGTCTG	(SEQ ID NO:775);
GCCCGTCTGT	(SEQ ID NO:776);	CCCGTCTGTT	(SEQ ID NO:777);
CCGTCTGTTG	(SEQ ID NO:778);	CGTCTGTTGT	(SEQ ID NO:779);
GTCTGTTGTG	(SEQ ID NO:780);	TCTGTTGTGT	(SEQ ID NO:781);
CTGTTGTGTG	(SEQ ID NO:782);	TGTTGTGTGA	(SEQ ID NO:783);
GTTGTGTGAC	(SEQ ID NO:784);	TTGTGTGACT	(SEQ ID NO:785);
TGTGTGACTC	(SEQ ID NO:786);	GTGTGACTCT	(SEQ ID NO:787);
TGTGTGACTC	(SEQ ID NO:788);	GTGTGACTCT	(SEQ ID NO:789);
TGTGACTCTG	(SEQ ID NO:790);	GTGACTCTGG	(SEQ ID NO:791);
TGACTCTGGT	(SEQ ID NO:792);	GACTCTGGTA	(SEQ ID NO:793);
ACTCTGGTAA	(SEQ ID NO:794);	CTCTGGTAAC	(SEQ ID NO:795);
TCTGGTAACT	(SEQ ID NO:796);	CTGGTAACTA	(SEQ ID NO:797);
TGGTAACTAG	(SEQ ID NO:798);	GGTAACTAGA	(SEQ ID NO:799);

111. A method for determining the pathogenicity of a strain of HIV-1 after said HIV-1 strain infects cells of an individual, said method comprising contacting a biological sample from said individual with a peptide corresponding to a deleted or truncated region of an HIV-1-derived protein and screening for the absence of antibody binding to said peptide, wherein the absence of antibody binding is indicative of a deletion or

- 282 -

118. Antibodies to the synthetic peptide defined in claim 117.

930604, p. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23

- 283 -

119. A method for determining the risk of an individual seropositive for HIV-1 developing symptoms of AIDS, said method comprising contacting antibodies from said patient with a synthetic peptide defined by SEQ ID NO:201 or a part or derivative thereof and detecting non-binding of antibodies to said peptide wherein the substantial absence of antibodies to said peptide is indicative of a low risk of the individual developing AIDS.

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950006, p100p100, HIV1 L2722-284

- 284 -

ABSTRACT

The present invention relates to non-pathogenic strains of HIV-1 and to components, parts, fragments and derivatives thereof and to genetic sequences derived therefrom and their use in the development of diagnostic and therapeutic compositions for the treatment and prophylaxis of AIDS and AIDS-related disorders. The present invention also relates to a method for attenuating pathogenic strains of HIV-1 by mutagenizing particular regions of the HIV-1 genome.

1/101

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GAACAGATTTGGAATAACATGACCTGGATGGAGTGGGACAGAGAAATTAA
*** ***** * ***** * ***** *
GAAGAGATTTGGGAGAACATGACCTGGATGCAGTGGGAAAAGAAATTCA
*** ***** * ***** * ***** *
GAAACAATTTGGGATAACATGACCTGGATCCACTGGGAAAGAGAAATTGA
*** ***** * ***** * ***** *
GAAACAATTTGGGATAACATGACCTGGATGCAGTGGGAAAGAGAAATTGA

GAAATTAA

8121

CAATTACACAAGCTTAATACACTCCTTAATTGAAGAAATCGCAAACCAGC
**** ***** * *** ***** ***** ***** *
CAATCACACAAATACATATACTCCTTACTTGAAAAATCGCAGAACCAAC
***** * ***** * ***** *
CAATTACACAACATAATATACACCTTAATTGAAGAAATCGCAGAACCAAC
***** ***** * ***** *
CAATTACACAACATAATATACACCTTAATTGAAGAAATCGCAGAACCAAC
***** ***** * ***** *
CAATTACACAAGATTAATATACAACCTTAATTGAAGAAATCGCAGAACCAAC

8171

FIGURE 1

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AAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTG

 AAGAAAAGAATGAACAAGAACTATTGGAATTGGATCAATGGGCAAGTTTG

 AAGAAAAAATGAACTAGAATTATTGGAATTGGATAAATGGGCAAATTTG

 AACAAAAAATGAACTAGAATTATTGGAATTGGATAAATGGGCAAATTTG

 AAGAAAAGAATGAACAAGACTTATTGGAATTAGATAAATGGGCAAGTTTG

8221

TGGAAATTGGTTTAAACATAACAAATTGGCTGTGGTATATAAAATTATTCAT

 TGGAAATTGGTTTGACATAACAAATGGCTGTGGTATATAAAATATTCAT

 TGGAAATTGGTTTAGTATATCAAACCTGGCTATGGTATATAAAATTATTCAT

 TGGAAATTGGTTTAGTATATCAAACCTGGCTATGGTATATAAAATTATTCAT

 TGGAAATTGGTTTGACATAACAAGTGGGCTGTGGTATATAAAATTATTCAT

8271

FIGURE 1

3/101

AATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTT

AATGGTAGTAGGAGGCTTGATAGGTTTAAGAATAGTTTTTGCTGTACTTT

AATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTACTGTACTTT

AATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTACTGTACTTT

AATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTAGCTGTACTTT

8321

SA8 SA9

SA10

CTATAGTCAATAGACTTACCCAGCCATATTCACCATTATCCTTTCAACACC

CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCGTTTCAGACC

CTATAGTTAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC

CTATAGTTAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC

CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC

8371

FIGURE 1

094673-000000

4/101

Tat termination NL43

CACCTCCCAATCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGA 8421
* * * * *
CTCCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA
* * * * *
CACCTCCCAACCCCGAAGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA
* * * * *
CACCTCCCAACCCCGAGGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA
* * * * *
CACCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA

AGGTGGAGAGAGAGACAGAGACAGATCCATTCGATTAGTGAACGGATCCT 8471
* * * * *
AGGTGGAGAGAGAGACAGAGACAGATCCACTCCATTAGTACACGGATTCT
* * * * *
AGGTGGAGAGAGAGACAGAGGCAGCTCCACTCGATTAGTGCACGGATTCT
* * * * *
AGGTGGAGAGAGAGGCAGAGGCAGCTCCACTCGATTAGTGCACGGATTCT
* * * * *
AGGTGGAGAGAGAGACAGAGACAGATCCAGTCGATTAGTGCACGGATTCT
D36P, C18S, C18M & C98H Tat termination

FIGURE 1

09146783-09090

[illegible]

8521

8571

6/101

ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAAATCTCCTACAGTATT

ACGCAGGGGATGGGAAGCCCTCAAATA1TGGTGGAACTCCTAAAGTATT

ACGCAGGGGATGGGAAGCCCTCAAATACTGGTGGAAATCTCCTGCAGTATT

ACGCGGGGGATGGGAAGCCCTCAAATACTGGTGGAAATCTCCTGCAGTATT

ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAAATCTCCTACAATATT

8621

NL43 Rev termination

GGAGTCAGGAACTAAAGAATAGTGCTGTAACTTGCTCAATGCCACAGCC

GGAGCCAGGAACTGCAGAAGAGTGCTGTTATCTTCTCAATGCCACCGCC

GGAGGCAGGAACTACAGAAGAGTGCTGTTAGCTTGTTCAATGGCAGGGCC

GGAGACAGGAACTACAGAAGAGTGCAGTTAGCTTGTTCAATGCCATAGCC

GGAGTCAGGAACTCAAGAAGAGTGCTATTAGCTTGTTCAATGCCACCGCC

8671

C183, C18M & C98H Rev termination

FIGURE 1

BBE060" E8294T60

7/101

ATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTATTACAAGCAGC

ATAGCAGTAGCTGAGGGGACAGATAGAGTTTATAGAAGTATTACAAAGAGC

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGCTTTACCAAGGGC

ATAGCAGTAGCTGAGGGGACAGATAGAGCTATAGAAGGATTACAAACACC

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGTATTACAAAGAGC

8721

incomplete, AGGGGACAGATAGAGTTCTAGAAGTATTACAAAGAGC
D36P Rev termination

TTATAGAGCTATTCGCCACATACCTAGAAGAATAAGACAGGGCTTGGA

TTATAGAGCTATCCTCCACATACCTAGAAGAATAAGACAGGGCCTCGAA

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGCTTAGAA

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGCTTAGAA

TTGTAGAGCTGTTCTCCACATACCTAGAAGAATAAGACAGGGCTTCGAA

TTATAGAGCCATTCTCCACATACCTAGAAGAATAAGACAGGGCTTCGAA

8771

FIGURE 1

00145783.00000

8/101

Env termination Nef start

```

GGATTTTGCTATAAGATGGGTGGCAAGTGGTCAAAAAGTAGTGTGATTGG      8821
*  *****  *****  *****  *****  *****  *  *
TGGCTTTGCTATAAAATGGGTGGCAAGTGAGCAAAAAGTAGTGTAGTCAG
**  *****  *****  *****  *****  *****  **  *
GGGCTTTGCTATAAAATGGGTGGCAAGTGGTCAGAAAGTAGTGTGGTTAG
**  *****  ***  *****
GGGCTTTGCTGTAAAATGGG-----
**  *  *****  *****  *****  *****  *****  *  *  *
GGGCTATGCTATAAAATGGGTGGCAAGTGGTTAAAAGTAGTATGGTTAG
*  ***  *****  *****  *****  *****  ****  *****  **  *
TGGCTTTNCTATAAAATGGGTGGCAAGTGGGCAAAAGGTAGTGTACTTAG
D36P Nef termination

```

nef duplication region

```

ATGGCCTGCTGTAAGGGAAAGAATGAGACGAGCTGAGCCAGCAGCAGATG      9871
**  **  **  *****  **  **  **
ATAGCATG-----CATCATAAG
*  ***  **
AAGGCATG-----
-----
*****  *****  *****  *****  *****  *
ATGGCCTGCTGTAAGGGAAAAAATGAAACAAGCTGAGCCAGCAGCAGAAG
*****  *****  *  *  *****  *****  *****  *
ATGGCAGGCTGTAAGGGAAAAA-TAAAACGAGCTGAGCCAGCAGCAGAAG

```

FIGURE 1

00145703-090300

9/101

GGGTGGGAGCAGTATCTCGAGACCTAGAAAAACATGGAGCAATCACAAGT
***** **

8921

GGGTGGGGGC-----

GGGTGGGAGCAATATCTCGAGACCTAGGAAAACATGGAGCAATCCCAAGT

GGGTGGGAGC-----

SIV_{mac239} IPTC

AGCAATACAGCAGCTAACAATGCTGCTTGTGCCTGGCTAGAAGCACAAGA

** ** ***** *

8971

-----CAACAATAACAATGCTGATCGTGCCTGGCTAGAAGCACAAGA

AGCAATACAACAATAACAATGCTAATTGTGCCTGGCTAGAAGCACAAGA

** ** ***** *

-----CAACAATAACAATTCTGGTTGCGCCTGGCTAGAAGCA-----

FIGURE 1

00146793-00099
00000-00000

10/101

GGAGGAAGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAA

9021

* * * * *

GAAGGAAGAAGCGGGTTTTCCAGTCAAACCTCAGGTA-----

* * * * *

-----TACCTTTAAGAC---

* * * * *

GGAGGAGGAAGTGGGTTTTCCAGTCAAACCTCAGGTACCTTTAAGACCAA

Poly purine tract

TGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

9071

* * * * *

-----GCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

* * * * *

-----AAGGCAGCTATAGATCTTAGCCGCTTTTTTAAAGAAAAGGGG

* * * * *

-----GATCTTAGCCACTTTTTTAAAGAAAAGGGG

* * * * *

* * * * *

TGACTTACAAG-----GCCACTTTTTTAAAGAAAAGGGG

* * * * *

-----CACTTTTTTAAAGAAAAGGGG

C18S nef termination

C18M and C98H nef Termination

FIGURE 1

001463-00000-EB/294160

11/101

[U3
GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATATCCTTGATCT

GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCCTAAAGAAGACAAGATATCCTTGATCT

GGACTGGAAGGGCTAATACGCTCCCAAAGAAGACAAGATATCCTTGATCT

9121

SA12

GTGGATCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACAC

TTGGATCTACCACACACAAGGCTACT-----
**** *****
GTGGGGCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACGACACAC

9171

FIGURE 1

00145793-090399
000000-000000

```

{..dyad symmetry..
{..NRT-1.....

```

-----ATCCACTGACTTTTGG, TGGTGCCTTCAATT

CAGGGCCAGGGACCAGATATCCACTGACCTTTGGATGGTGCCTGCAACGA

FIGURE 1

13/101

NF-AT

CAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAGAGAG
*** *****

9321

CAGATTGTT-----
*** *****

CAGATTGTT-----
*** *****

CAGATTGTT-----

*** *****

CAGACTGTT-----

USF

<-- NRE]

AAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACGTGGCC

9371

* * *
-----CCGTTTGTT

* *
-----CTGCT

-----A

FIGURE 1

00467-00000
00000-00000

14/101

TCF-1α

Nef termination

CGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTA 9421
 * * * * *
 CTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAAGGCGGCGTGGCCTG
 * * * * *
 CCGTTGGGGACTTTCCA, , , , , GGAGACGTGGCCTGAGTGATAAGCCG
 * * * * *
 TGCTCAGCTGGGGACTTTCCAGAAGGCGCGCCTGAGTGACTAAGCCCCG
 * * * * *
 CAGAGTGTGGGGACTCTCCACAACAGAGTGTGGGGACTTTCCAAGGAGGC
 * * * * *
 ----CCGTTGGGGACTTTCCAAGGAGGCGTGGCCTGAGTGACTAAGTTCC
 D36P, C18S, C18M & C98H extra NFκB
 D36P & C98H extra NFκB

NFκB	NFκB	Sp1	
CAAGGGACTTTCCG, , , , , , , , , ,	CTGGGGACTTTCCAG, GGAGGCGTGGC		9461
* * * * *	* * * * *	* * * * *	
GGTGACTAGTTCCG, , , , , , , , , ,	GTGGGGACTTTCCAA, GAAGGCGCGGC		
* * * * *	* * * * *	* * * * *	
CTGGGGACTTTCCGAAGAGGCGTGACGGGACTTTCCAA, GGCGACGTGGC			
* * * * *	* * * * *	* * * * *	
TTGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCAA, GCAGGCGTGGC			
* * * * *	* * * * *	* * * * *	
GTGGCCTGAGTGACTAAGTTCCGTTGGGGACTTTCCAA, AAAGGCGAGGC			
* * * * *	* * * * *	* * * * *	
GTTGGGACTTTCCAAGGAGGC, , GCGGGGACTTTCCAA, GGAGGCGCGGC			
C18S & C18M NFκB	NFκB	Sp1	
D36P and C98H 3'-half NFκB			

FIGURE 1

15/101

Sp1	Sp1	TATA box	
CTGGGCGGGACTGGGGAGTGGCGAGCCC,	TCAGATGCTGCATATAAGCAG		9510
*****	*****		
CTGGGCGGGACTGGGGAGTGGCGAGCCC,	TCAGATGCTGCATATAAGCAG		
*****	*****		
CTGGGCGGGACTGGGGAGTGGCGAGCCC,	TCAGATGCTGCATATAAGCAG		
*****	*****		
CTGGGCGGGACTGGGGAGTGGCGAGCCC,	TCAGATGCTGCATATAAGCAG		
*****	*****		
CTGGGCGGA-CTGGGGAGTGC-GAGCC-,	TCAGATGCTGCATATAGGCAG		
*****	*****		
CTGGGCGGGACTGGGGAGGGGCGAGCCC,	TCAGATGCTGCATATAAGCAG		

Sp1 Sp1

U3		R	TAR	
CTGCTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG				9560
*****	*****			
CTGCTTTCTGCTGTACTGGGTCTCTCGGGTTAGACCAGATCTGAGCCTG				
*****	*****			
CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG				
*****	*****			
CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG				
*****	*****			
CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG				
*****	*****			
CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCT..incomplete				

FIGURE 1

094457-0000

16/101

	Sp1	Sp1	TATA box	
NL43	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			9510

D36P	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			

C18S	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			

C18M	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			

C98H	CTGGGCGGA-CTGGGGAGTGC-GAGCC-, TCAGATGCTGCATATAAGCAG			

C54H2	CTGGGCGGGACTGGGGAGGGGCGAGCCC, TCAGATGCTGCATATAAGCAG			

Sp1 Sp1

	U3	R	TAR	
NL43	CTGCTTTTTCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			9560

D36P	CTGCTTTCTGCTGTACTGGGTCTCTCGGGTTAGACCAGATCTGAGCCTG			

C18S	CTGCTTTCTGCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			

C18M	CTGCTTTCTGCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			

C98H	CTGCTTTCTGCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			

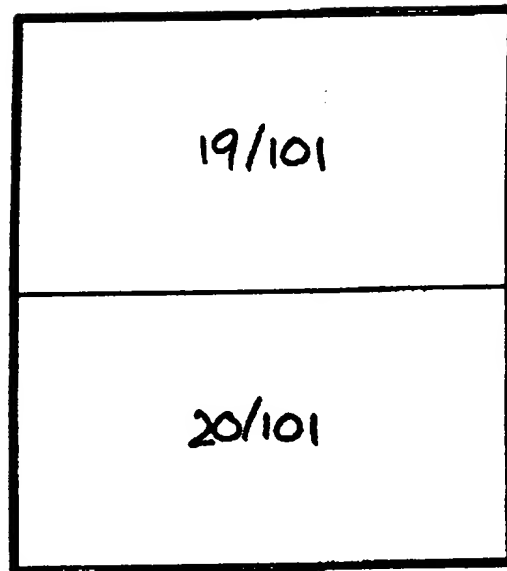
C54H2	CTGCTTTCTGCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCT..incomplete			

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18/101

FIGURE 2



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19/101

FIGURE 2A

86

635 NL43 73 PTSQSRGDPPTGPKE#
 636 D36P BMC PSSQPRGDPPTGPKEKKKVERETETDPLD#
 637 C18 HIV_{Stv} PTSQPRRDPTGQKESKKKVERETEAAPLD#
 C18 HIV_{MBC} PTSQPRRDPTGQKESKKKVERETEAAPLD#
 C98 HIV PTSQPRRDPTGQKESKKKVERETETDPVD#

FIGURE 2B

65

638 NL43 26 DPPPNEGTRQARRNRRRRWRERQRQIHSISERILSTYLG
 639 D36P BMC DPPPNEGTRQARRNRRRRWRERQRQIHSISTRILSTFLG
 640 C18 HIV_{Stv} DPPPNEGTRQARRNRRRRWRERQRQIHSISARILSTFLG
 C18 HIV_{MBC} DPPPNEGTRQARRNRRRRWRERQRQIHSISARILSTFLG
 C98 HIV DPPPNEGTRQARRNRRRRWRERQRQIQSISARILSTFLG

FIGURE 2B

NL43 RSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVGSPQILVE 105

D36 PBMC RPEEPVPLPLPPLERLTLDNCNKDCGTSGTQGMGSPQILVE

C18 HIV_{stv} RPEESVPLQLPPLERLTLDNCNEDCGTSGTQGMGSPQILVE

C18 HIV_{mbc} RPEESVPLQLPPLERLTLDNCNEDCGTSGTQGMGSPQILVE

C98 HIV RPEEPVPLQLPPLERLTLDNCNEDCGTSGTQGVGSPQILVE

20/101

NL43 SPTVLESGTKE# 116

D36PBMC PPKVLEPGTAEECCYLAQCHRHSSS#

C18 HIV_{stv} SPAVLEAGTTEECC#

C18 HIV_{mbc} SPAVLEAGTTEECC#

C98 HIV SPTILESGTQECCY#

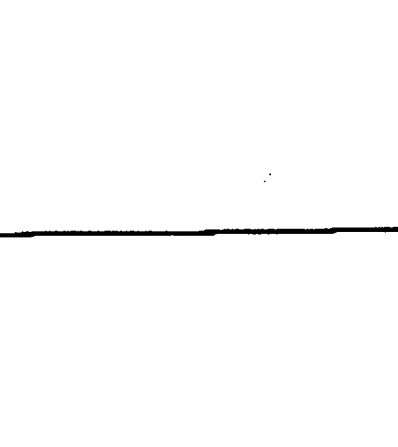
[illegible]

FIGURE 3

611 NL43
 612 D36P BMC
 613 C18 HIV_{scv}
 C18 HIV_{MBC}
 C98 HIV

EQIWNNTMTMWDREINNNTSLIHSLEESQSQEKNEQELLELDKWASL
 BEIWENMTMQWEKEIHNHTKYIYSLLEKSQSQEKNEQELLELDQWASL
 ETIWDNMTMQWEREIDNYTNIITYLLEESQSQEKNELELELDKWANL
 EINNNTYRTIYNLLEESQSQEKNEQDLELDKWASL

639

NL43
 D36 P BMC
 C18 HIV_{scv}
 C18 HIV_{MBC}
 C98 HIV

WNVFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQT
 WNVFDITKWLWYIKLFIMVVGGLIGLRIVFAVLSIVNRVRQGYSPLSFQT
 WNVFSISNWLWYIKLFIMVVGGLVGLRIVFTVLSIVNRVRQGYSPLSFQT
 WNVFDITSGLWYIKLFIMIVGGLVGLRIVLAVLSIVNRVRQGYSPLSFQT

689

FIGURE 3

NL43	HLPIPRGPDPRPEGIEEGGERDRDRSIRLVNGSLALIWDLRLSLCLFSYH	739
D36 PBMC	LLPTPRGPDPRPEGIEEGGERDRDRSTRLVHGFALFWDDLRLSLCLFLYH	
C18 HIV _{stv}	HLPTPKGPDPRPEGIEEGGERDRGSSTRLVHGFALFWDDLRLSLCLFSYH	
C18 HIV _{mbc}		
C98 HIV	HLPTPRGPDPRPEGIEEGGERDRDRSSRLVHGFALFWVDLRLSLCLFSYH	
NL43	RLRDLLLIVTRIVELLGRRGWEALKYWNLLQYWSQELKNSAVNLLNATA	789
D36 PBMC	HLRDLLLIVTRIVELLGRRGWEALKYWNLLKYWSQELQKSATIVLLNATA	
C18 HIV _{stv}	HLRDLLLIVTRIVELLGRRGWEALKYWNLLQYWRQELQKSAVSLFNATA	
C18 HIV _{mbc}		
C98 HIV	RLRDLLLIVTRIVELLGRRGWEALKYWNLLQYWSQELKKSATSLFNATA	
NL43	IAVAEGTDRVIEVLQAYRAIRHIPRIRQGLERILL#	839
D36 PBMC	IAVAEGTDRVIEVLQAYRAIRHIPRIRQGLEMALL#	
C18 HIV _{stv}	IAVAEGTDRVIEALRRAYRAIRHIPRIRQGLERALL#	
C18 HIV _{mbc}		
C98 HIV	IAVAEGTDRVIEVLQACRAVLHIPRIRQGFERAML#	

24/101

FIGURE 4

NL43	MGGKWSKSSVIGWPAVRERMRRRAEPAADGVGAVSRDLEKHGAITSSNTAA ***	50
D36 PBMC	MGGK# *****	4
C18. HIV _{STV}	MGGKWSSESVRRHVPLRQGSYRS# *	24
C18 HIV _{MBC}	MRILATF# *****	7
C98 HIV	MGGKWLKSSMVRWPAVREKMKQAEPAEAGVGVAISRDLGKHGAIPSSNTTT *****	50
NL43	NNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGL ***	100
C98 HIV	NNANCAWLEAQEEEEVGFPVKPQVPLRPMTYKATF# *****	85
NL43	IHSQRRQDILDNLWYHTQGYFPDQNYTPGPGVRYPLTFGWCYKLVPEP	150
NL43	DKVEZANKGENTSLHPVSLHGMDDPEREVLEWRPDSRLAFHHVARELHP	200
NL43	EYFQNC*	206

FIGURE 5

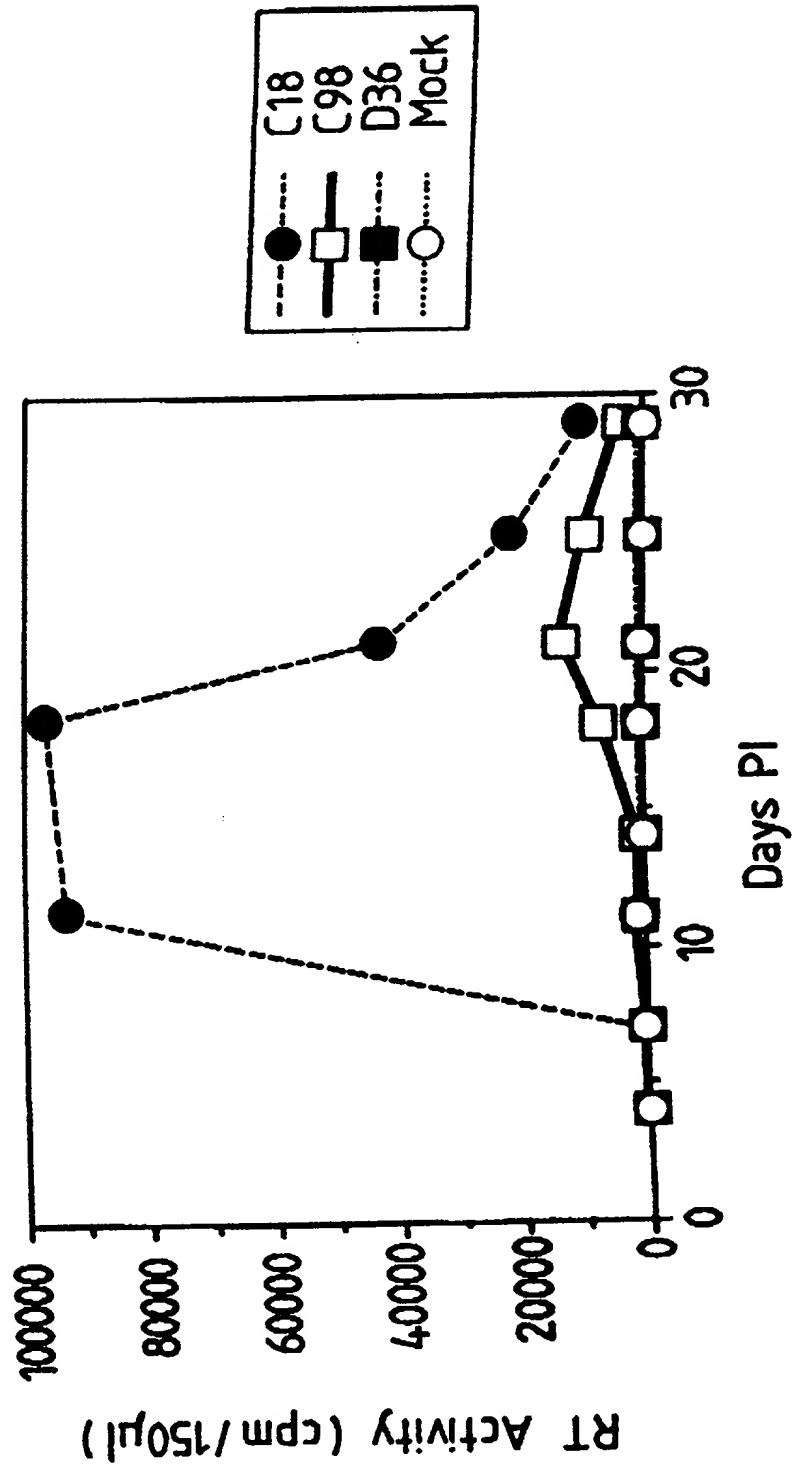
	NFkB	NFkB
9419 NL43	CGAGCTTGCTACAAAGGGACTTTCC,,GCTGGGACTTTCCAGGGA ** ***** *	
D36 PBMC	ACTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAAAGGC * ** * ***** **	
C18 HIV _{stv}	ΔCCGTTGTCCGTTGGGGACTTTCCA-GGA * ***** *	
C18 HIV _{mbc}	ΔCTGCTTGCTCAGCTGGGGACTTTCCA-GAA * * * * *	
C98 HIV	ΔACAGAGTGTGGGGACTCTCCACAACAGAGTGTGGGGACTTTCCAAGGA * ***** **	
C54 PBMC	ΔCCGTTGGGGACTTTCCAAGGA NFkB	
	Sp1	Sp1
NL43	GGCGTGGCCTGGGGGACTGGGGAGTGGCG-AGCCCTCA ***** *	9492
DC36 PBMC	GGCGTGGCCTGGGTGACTAGTTCCGGTGGGG-ACTTTCCA * ***** *	
C18 HIV _{stv}	GACGTGGCCTGAGTGACTAAG-CCGCTGGGG-ACTTTCCG *** ***** *	
C18 HIV _{mbc}	GGCGGGCCTGAGTGACTAAGCCCGTTGGG-ACTTTCCG ***** *	
C98 HIV	GGCGTGGCCTGAGTGACTAAGTTCCGTTGGGGACTTTCCA ***** *	
C54 PBMC	GGCGTGGCCTGAGTGACTAAGTTCCGTTGGGGACTTTCCA Sp1 3' half NFkB NFkB	

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26/101

FIG 6

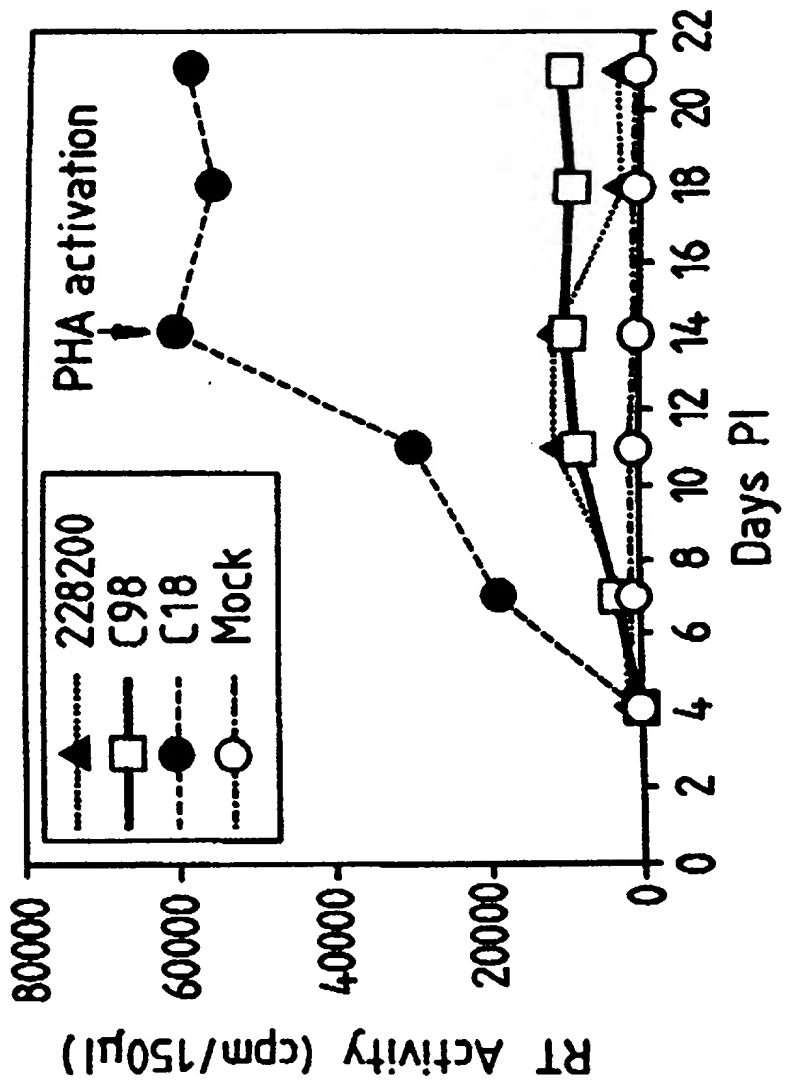
**Replication of Sydney Asymptomatic
Patients Isolates in PHA-stimulated PBMCs**



27/101

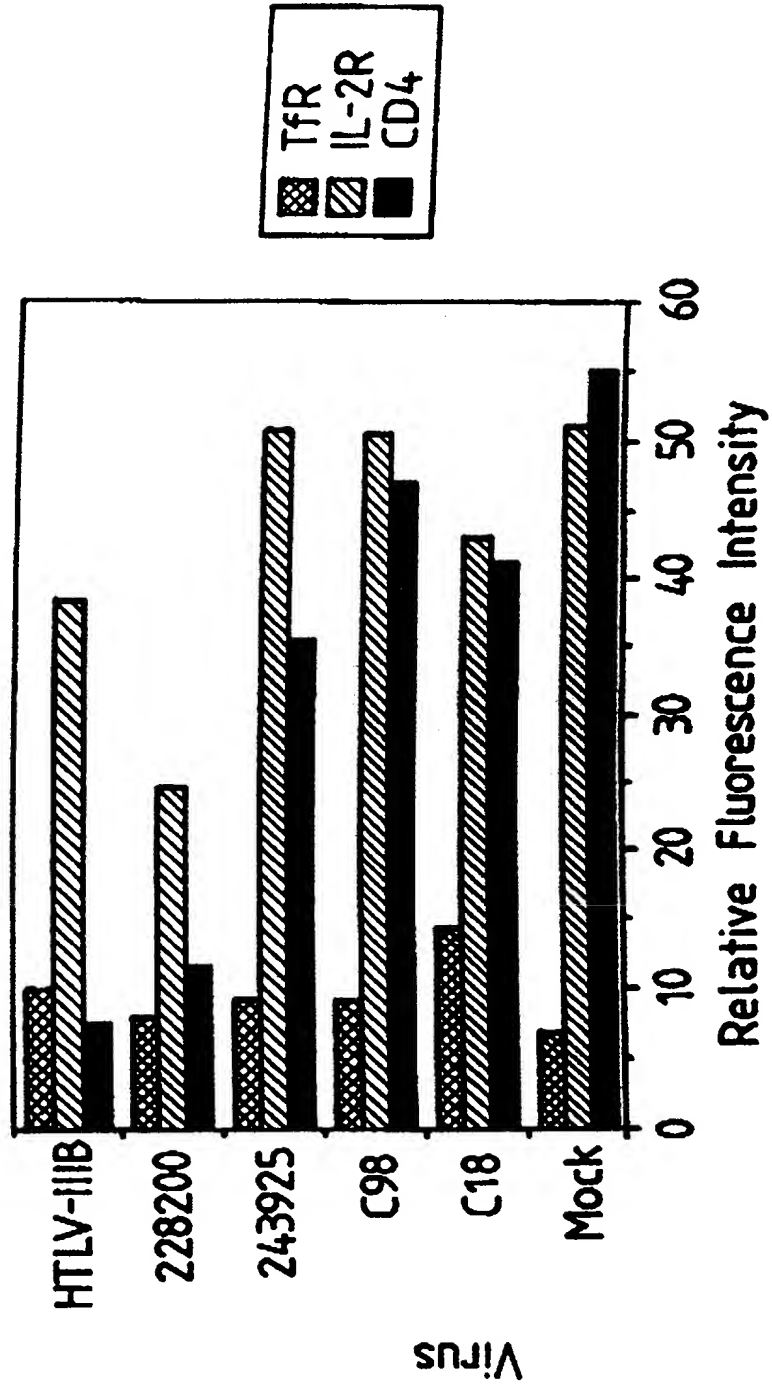
FIG 7

Replication of Sydney Asymptomatic
Patient Isolates in non-PHA stimulated PBMCs



28/101

FIG 8



29/101

FIGURE 9

30/101
31/101
32/101
33/101
34/101
35/101

09146783-090308

FIGURE 9

30/101

TGGAAGGGCTAATTCACCTCACGGAAAAGACCAGTTGAACCAG
AAGAAGATAGAAGAGGCCATGAAGAAGAAAACAACAGATTGT
TCTGCTTGCTCAGCTGGGGACTTTCCAGAAGGCGCGGCTGA
GTGACTAAGCCCCGTTGGGGACTTTCCGAAGAGGCATGAAGG
GACTTTCCAAGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTG
GCGAGCCCTCAGATGCTGCATATAAGCAGCTGCTTTCTGCCT
GTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGC
TCTCTGGCTAGCTAGGGAACCCACTGCTTAAGCCTCAATAAA
GCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGT
GTGACTCTGGTATCTAGAGATCCCTCAGACCATTTTAGTCCG
TGTGGAAAATCTCTAGCAGTGGCGCCCCGAACAGGGACTTGAA
AGCGAAAGGAAAACCAGAGGAGCTCTCTCGACGCAGGACTCG
GCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACT
GGTGAGTACGCCGAAAATTTTGACTAGCGGAGGCTAGAAGGA
GAGAGATGGGTGCGAGAGCGTCAATATTAAGCGGGGGAAAAT
TAGATAGATGGGAGAAAATTCGGTTAAGGCCAGGAGGAAAGA
AAAAGTATAAATTAAAACATATAGTATGGGCAAGCAGGGAGC
TAGAACGATTTCGCAGTCAATCCTGGCCTGTTGGAAACATCAG
AAGGCTGTAGACAAATACTGGGACAGTTACACCCGTCCCTTC
AGACAGGATCAGAAGAACTTAAATCAGTATATAATGCAGTAG
CAGTCCTCTATTGTGTGCATCAAAACATAGACATAAAGGACA
CCAAGGAAGCTTTAGAAAAGATAGAGGAAGAGCAAAACAAAT
GTAAGAAAAAAGCACAGCAAGCAGCAGCACAGCAAGCAGCAG
CTGGCACAGGAAACAGCAACCCGGTCAGCCAAAATTACCCTA
TAGTACAGAACATGCAGGGGCAAATGGTACATCAGGCCATAT
CACCTAGAACTTTAAATGCATGGGTAAAAGTAATAGAAGAGA
AGGCTTTCAGCCCAGAGGTAATACCCATGTTTTTCAGCATTAT
CAGAAGGAGCCACCCACAAGATTTAAACACCATGCTAAACA
CAGTGGGGGGACATCAAGCAGCTATGCAAATGTTAAAAGAGA
CCATCAATGAGGAAGCTGCAGAATGGGATAGATTACATCCAG
CGCAGGCAGGGCCTGTTGCACCAGGCCAGATGAGAGACCCAA
GGGGAAGTGACATAGCAGGAACTACTAGTACCCTTCAGGAAC
AAATAGGATGGATGACAGGTAATCCAGCTATCCCAGTAGGAG
AAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
TAAGGATGTATAGCCCTATCAGCATTCTGGACATAAAACAAG
GACCAAAGGAACCCCTTTAGAGACTATGTAGACCGGTTCTATA
AAACTCTAAGAGCCGAGCAAGCTACACAGGAGGTAAAAAATT
GGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATT
GTAAGACTATTTTAAAGCATTGGGACCAGCAGCTACACTAG

FIGURE 9

3/101

AAGAAATGATGACAGCATGTCAGGGAGTGGGAGGACCCAGCC
ATAAAGCAAGAGTTTTTGGCAGAAGCAATGAGCCAAGCAACAA
ATGCAGCTACTGTAATGATGCAGAGAAGCAATTTTAGAAACC
AAAGAAAGAATGTTAAGTGTTCATTTGTGGCAAAGAAGGGC
ACATAGCCAGAAATTGCAGGGGCTCCTAGGAAAAGGGGCTGTT
GGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTG
AGAGACAGGCTAATTTTTTTAGGGAAAATCTGGCCTTCCCACA
AGGGGAGGCCAGGGAACTTTCTTCAGAGCAGGCCAGAACCAA
CAGCCCCCTCTCCAGGGCAGGCCGGAGCCATCAGCCCCGCCAG
AAGAGAGCTTCAGGTTTGGGGAGGAGACAACAACCTCCCTCTC
AGAAGCAGGAGCCGATAGACAGGGACAGGGATCTGTATCCTT
TAGCTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCAC
AATAAAGATAGGGGGGCAGCTGAAGGAAGCTCTATTAGATAC
AGGAGCAGATGATACAGTATTAGAAGACATGCATTTGCCAGG
AAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTAT
CAAAGTAAACAATATGATGAAATTCTTGTAGAAATCTGTGG
ACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGT
CAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTTGCAC
TTTAAATTTTCCCATTAGTCCTATTGAAACTGTACCAGTACA
ATTAAAGCCAGGAATGGATGGCCCAAAGGTTAAACAATGGCC
ATTGACAGAAGAGAAAATAAAAGCATTAGTAGAAATTTGTAC
AGAAATGGAAAAGGAAGGAAGATTTCAAAAATTGGGCCTGA
AAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGA
TGGTACTAAATGGAGAAAATTAGTAGATTTTCAGAGACCTTAA
TAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACC
ACATCCCTCAGGATTAAAAAAGAAAAAATCAGTAACAGTACT
GGATGTGGGTGATGCATACTTTTCAGTTCCCTTAGATGAAAA
CTTCAGGAAGTATACTGCATTTACCATACTAGTATAAATAA
TGAGACACCAGGGATTAGATATCAGTACAATGTGCTTCCACA
GGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGAC
AGAATCTTAGAGCCTTTTAGAAGACAAAATCCAGACATAGT
TATCTATCAATACATGGATGACTTGTATGTAGGATCTGATTT
AGAAATAGGACAGCATAGAATAAAAATAGAGGAACTGAGACA
ACATCTGTTGAAGTGGGGATTTACCACACCAGACAAAAGCA
TCAGAAAGAACCCCATTCCTTTGGATGGGTATGAACTCCA
TCCTGATAAATGGACAGTGCAACCTATAGTACTGCCAGAAAA
AGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGTAA
ATTAAATTGGGCAAGTCAGATTTACCCAGGAATTAAAGTAAG
GCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGA

FIGURE 9

32/101

AGTAATACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGA
AAACAGGGAAATTCTAAGAGAACCAGTACATGGAGTGTATTA
TGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGA
GCAAGGCCAATGGACATATCAAATTTATCAAGATCAATTTAA
AAATCTAAAAACAGGAAAGTATGCAAGATTGAGGGGTGCCCA
CACTAATGATGTAAAACAATTTCCAGAGGCAGTGCAAAAAT
AGCCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATT
TAGACTACCCATACAAAAGAAACATGGGACGCATGGTGGAC
AGAGTATTGGCAAGCCACCTGGATTCTTGAGTGGGAGTTTGT
CAATACCCCTCCCCTAGTAAAATTATGGTACCAGTTAGAAAA
AGAACCCATAATAGGAGCAGAACTTTCTATGTAGATGGGGC
AGCTAACAGAGAGACTAAATTAGGAAAAGCAGGATATGTTAC
TGACAGAGGAAGACAAAAGTTGTCTCCCTAACTGACACAAC
AAATCAGAAGACTGAGTTACAAGCAATTCATCTAGCTTTGCA
GGATTCAGGATTAGAAGTAAACATAGTAACAGACTCACAGTA
TGCATTAGGAATCATTCAAGCACACCAGATAAAAGTGAATC
AGAAATAGTCAATCAAATAATAGAGCAATTAATAAAAAAGGA
AAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGG
AGGGAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAG
GAAAATACTATTTTTTAGATGGAATAGATAAGGCACAAGAAGG
CCATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGG
TTTTAACCTGCCACCTATAGTAGCAAAAGAAATAGTAGCCAG
CTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACA
AGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACA
TCTAGAAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAG
TGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCA
GGAAACAGCATACTTTATCTTAAAATTAGCAGGAAGGTGGCC
AGTAAACACAATACATACAGACAATGGCGGCAATTTTCATCAG
TACCACGGTTAAGGCCGCCTGTTGGTGGGCAGGGATCAAGCA
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GAAAGGACCAGCAAACTTCTCTGGAAAGGCCGAAGGGGCAGT
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TTGTGGGTACAGTCTATTATGGGGTACCTGTGTGGAGAGAA
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ACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAG
ATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTGAAG
CCATGTGTAAAATTAACCCCACTCTGTGTTTCTTTAAATTGC
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AGCGAGAAACCGAAGGGGACAGGGGAAATAAAAAACTGCTCT

FIGURE 9

34/101

TTCAATATCACCACAAGCATAAGAGATAAGGTGCAGAAACAA
TATGCACTTTTTTATAGCCTTGATGTAGTACCAATGGATGAT
AATGATAATAGTACAAGCTATAGGTTAATAAGTTGTAACACC
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ATTCCCATACATTATTGTGCCCCGGCTGGTTTTTGCGATTCTA
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ACTTTAGAACAGATAGCTAGAAAATTAAGAGAACAATTTGAG
AATAAAACAATAGTCTTTAAGCCATCCTCAGGAGGGGACCCA
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AATGGTACTTGGGTTAATGGTACTTGGAGTAGTAATAATACG
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GTACAAGTTGAACCATTAGGAGTAGCACCCACCAAGGCAAAG
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TTGTCTGGTATAGTGCAGCAGCAGAACAATCTGCTGAGGGCT
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CTAAGGGATCAACAGCTCCTGGGACTTTGGGGTTGCTCTGGA
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AGTAATAAATCTCTGGAAACAATTTGGGATAACATGACCTGG
ATGCAGTGGGAAAGAGAAATTGACAATTACACAAACATAATA
TACACCTTAATTGAAGAATCGCAGAACCAACAAGAAAAAAT
GAACTAGAATTATTGGAATTGGATAAATGGGCAAATTTGTGG
AATTGGTTTAGTATATCAAACCTGGCTATGGTATATAAAATTA
TTCATAATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGTT

FIGURE 9

35/101

TTTACTGTACTTTCTATAGTTAATAGAGTTAGGCAGGGATAC
TCACCATTATCGTTTCAGACCCACCTCCCAACCCCGAAGGGA
CCCGACAGGCCAGAAGGAATCGAAGAAGAAGGTGGAGAGAGA
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CACCACCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTG
GAACTTCTGGGACGCAGGGGATGGGAAGCCCTCAAATACTGG
TGGAATCTCCTGCAGTATTGGAGGCAGGAACTACAGAAGAGT
GCTGTTAGCTTGTTCAATGGCACGGCCATAGCAGTAGCTGAG
GGGACAGATAGAGTTATAGAAGCTTTACGAAGGGCTTATAGA
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AGGGCTTTGCTATAAAATGGGTGGCAAGTGGTCAGAAAGTAG
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GAAGAGGCCATGAAGAAGAAAACAACAGATTGTTCTGCTTGC
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CCCCGTTGGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCA
AGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCT
CAGATGCTGCATATAAGCAGCTGCTTTCTGCCTGTACTGGGT
CTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCT
AGCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCCT
GAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTG
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TCTCTAGCA

trends in CD3 count since seroconversion

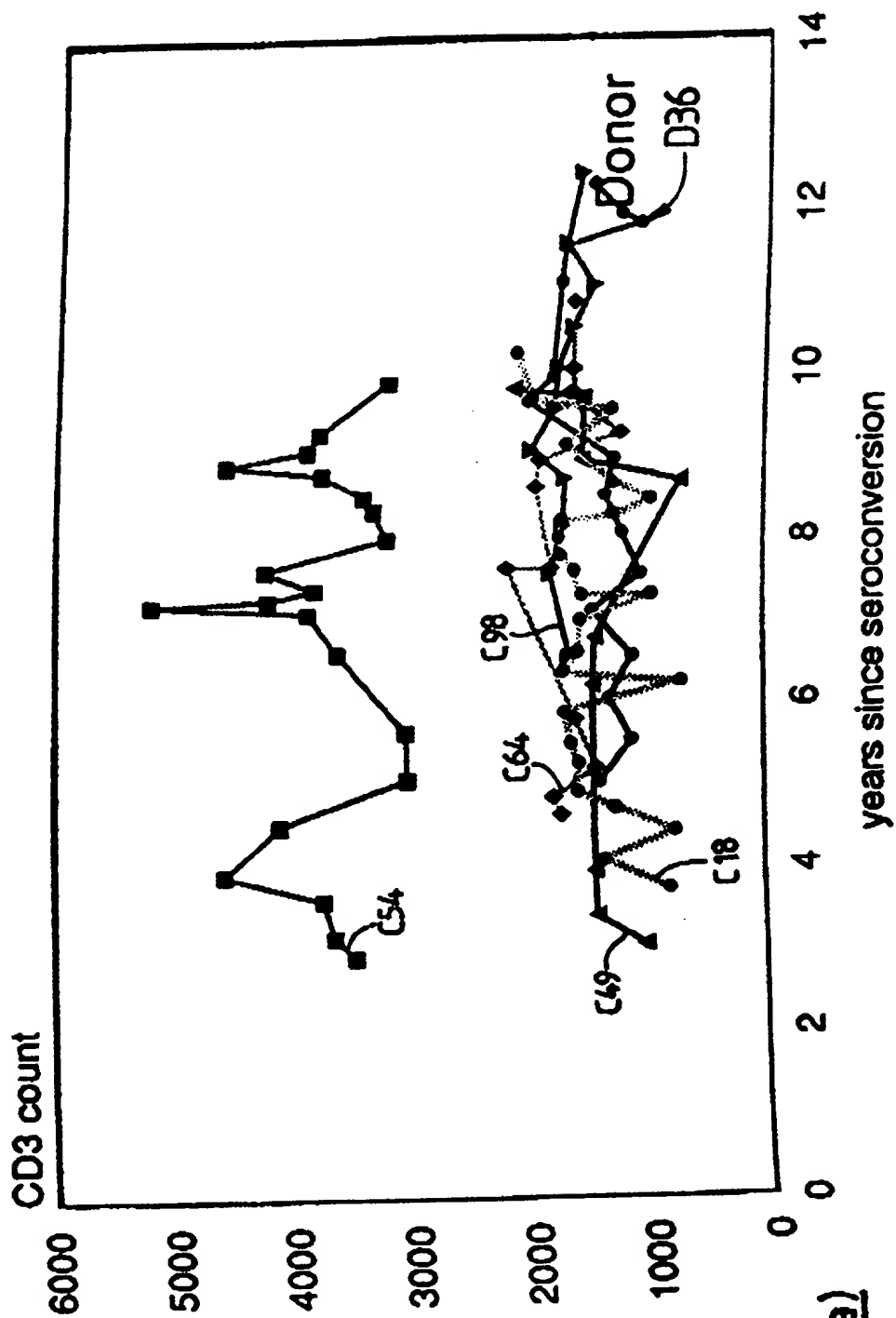


FIG 10(a)

FIG 10(b)(i) trends in CD4 count since seroconversion

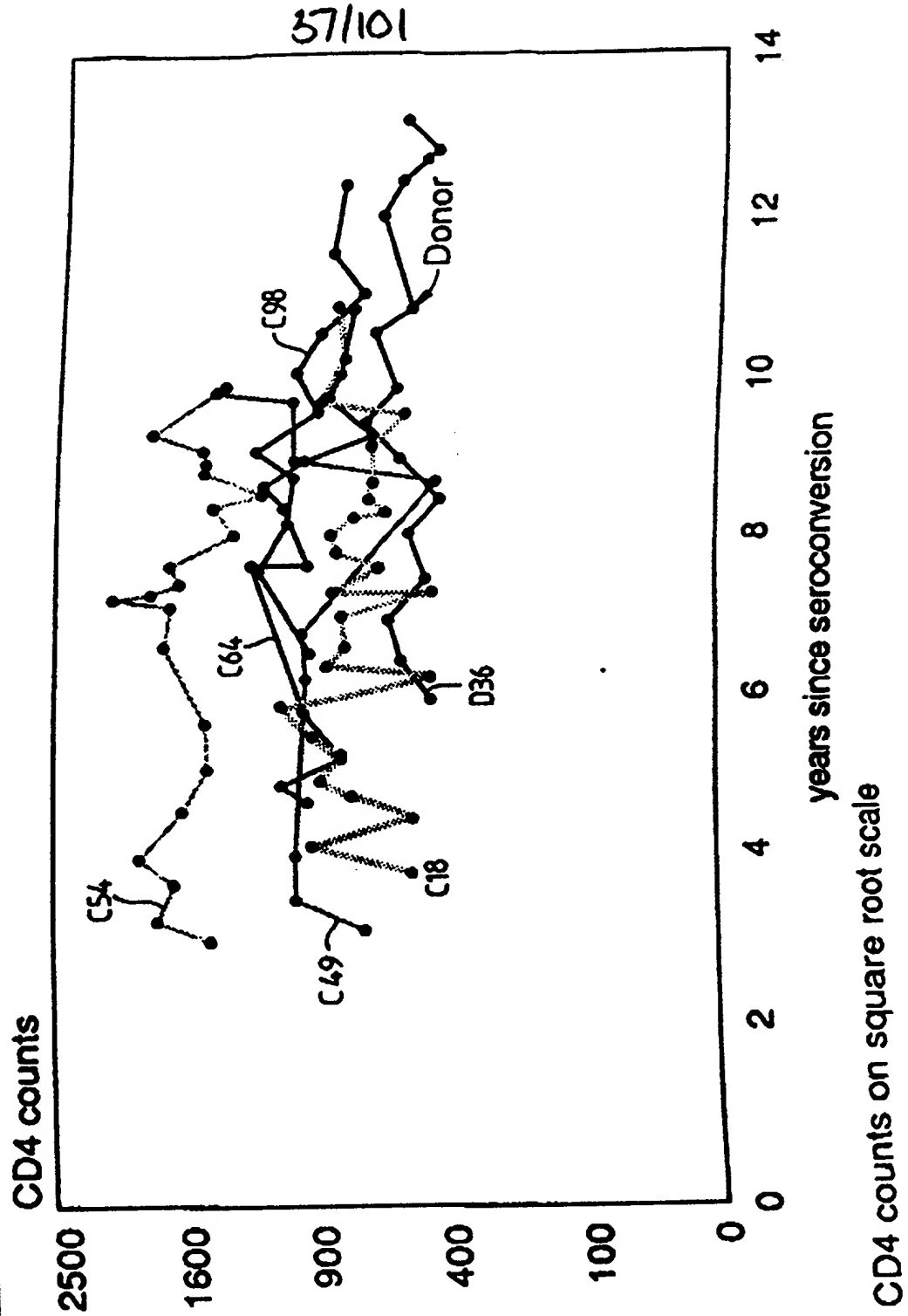
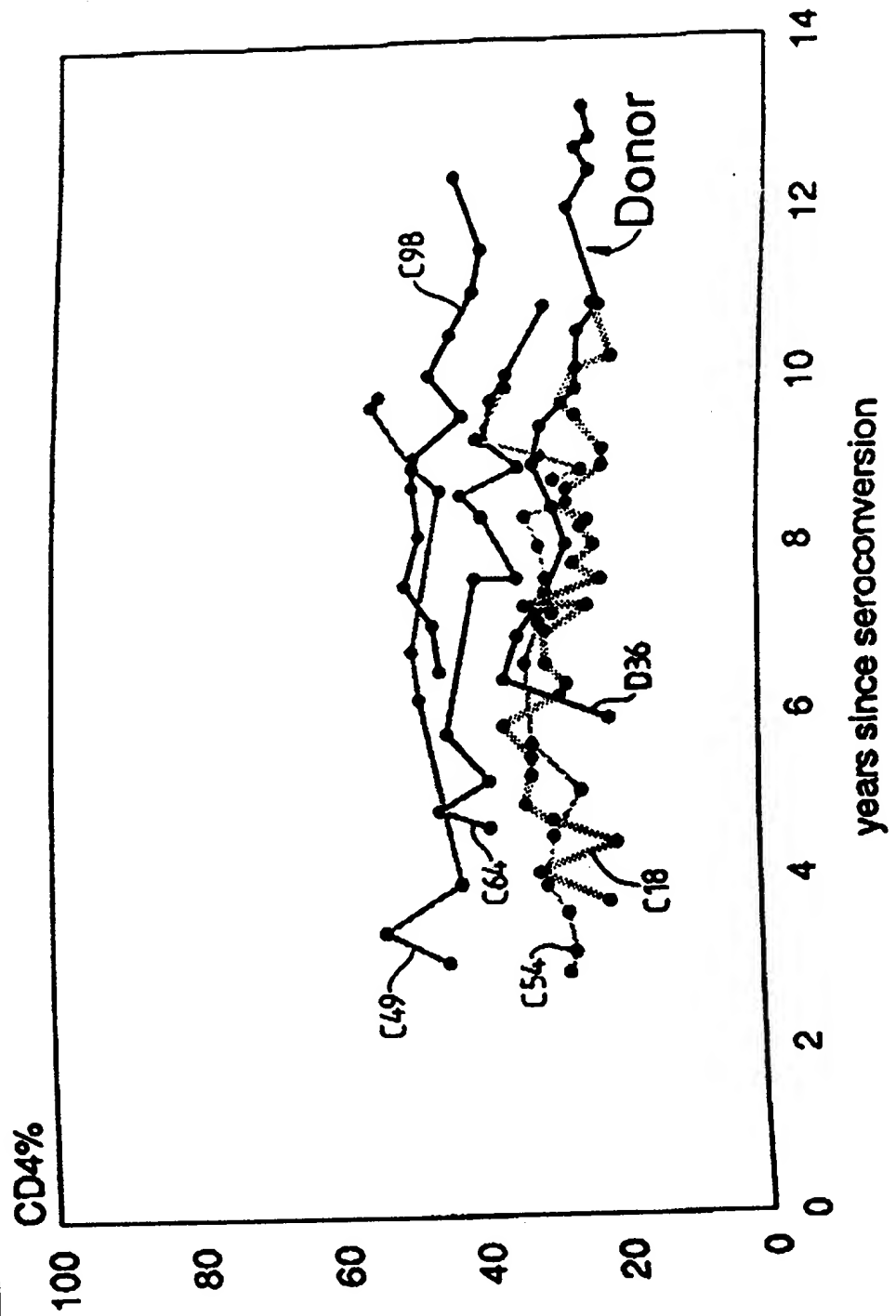


FIG 10(b)(ii) trends in CD4% since seroconversion



39/101

FIG 10(c)(i) trends in CD8 since seroconversion

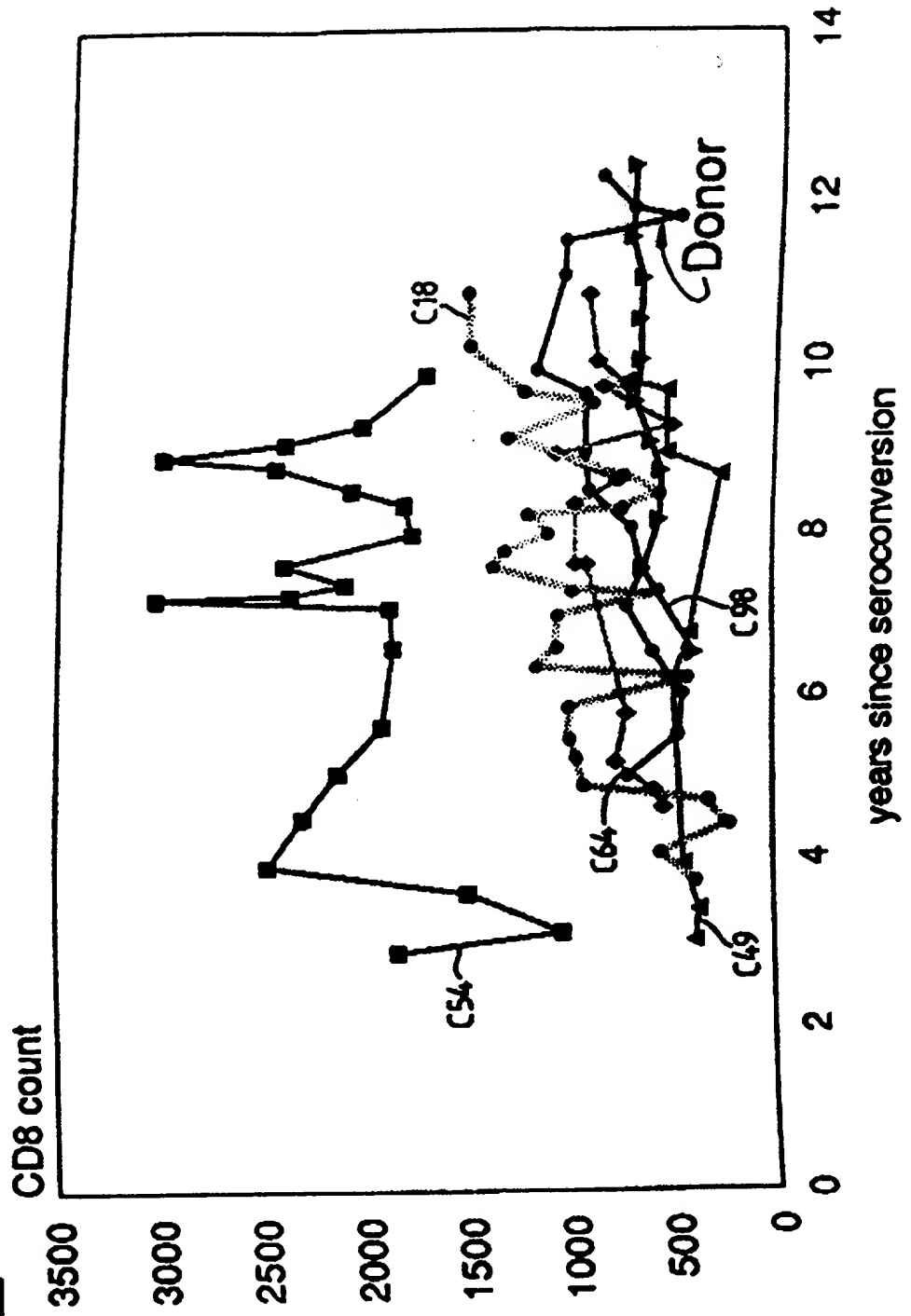


FIG 10 (c) (ii)

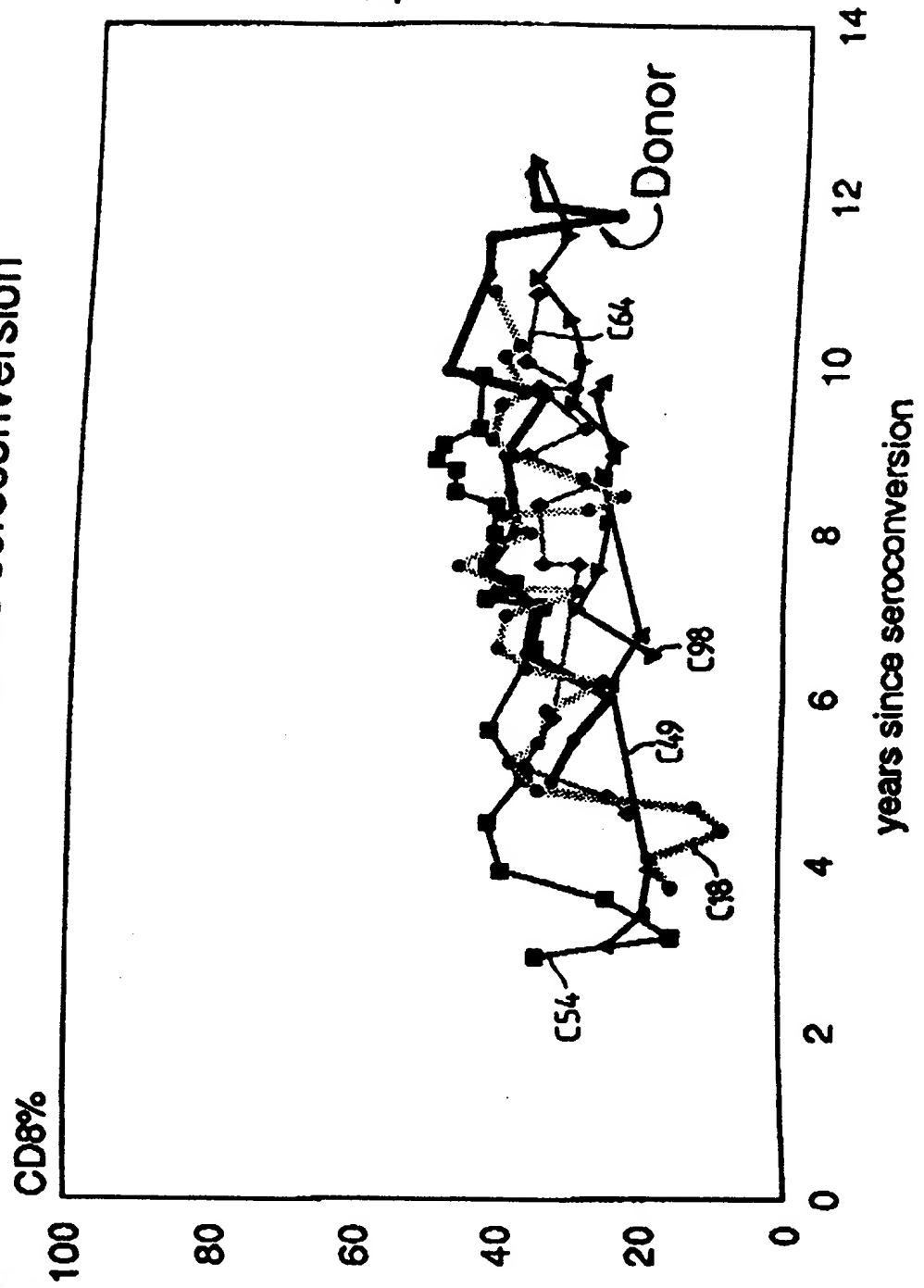


FIG 10(d)

trends in lymphocyte count since seroconversion

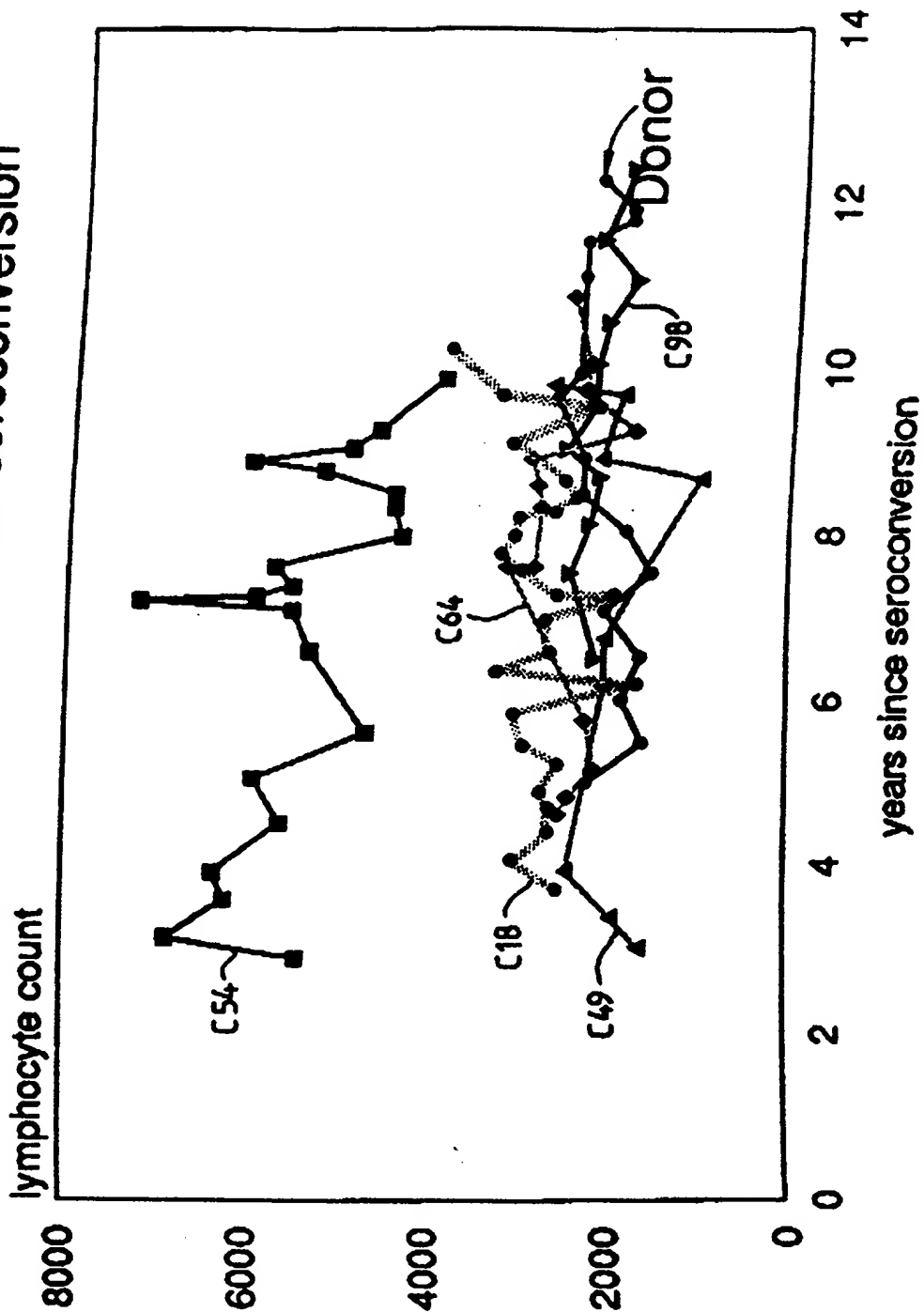


FIG 10(e) trends in CD4:CD8 ratio count since seroconversion

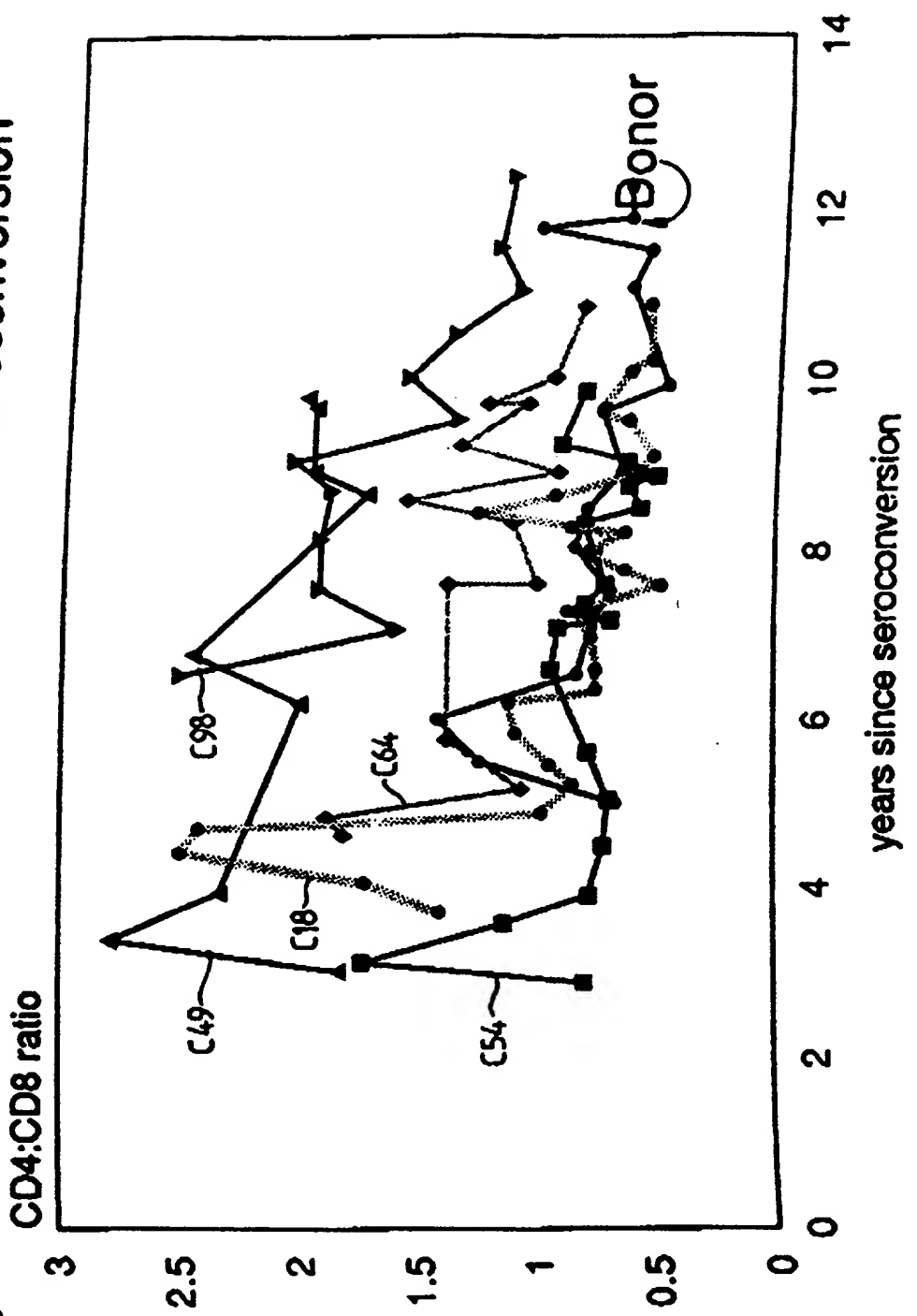
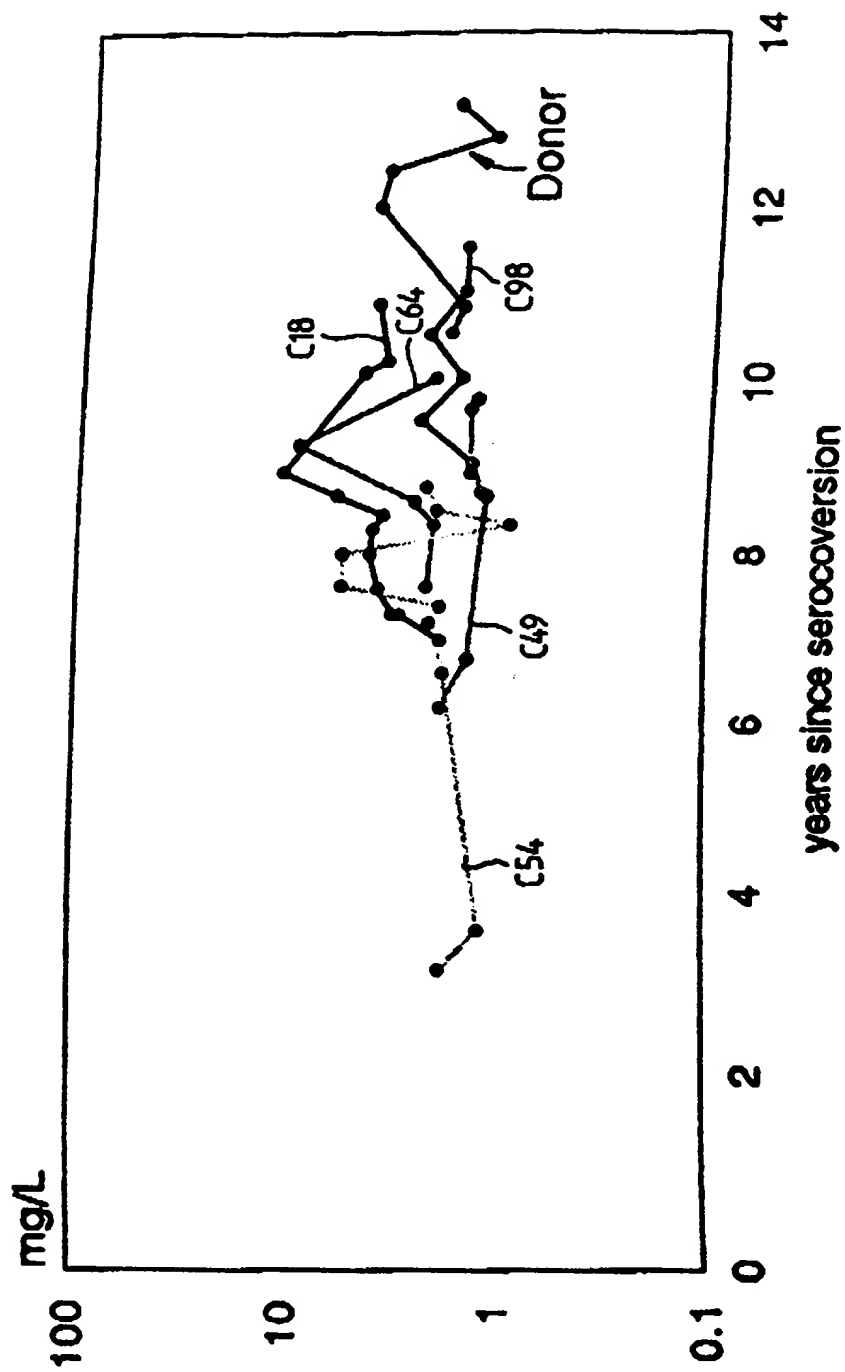


FIG 10 (f)
trends in beta-2 microglobulin since seroconversion



beta-2 microglobulin plotted on a log scale

44/101

FIG 10(g)

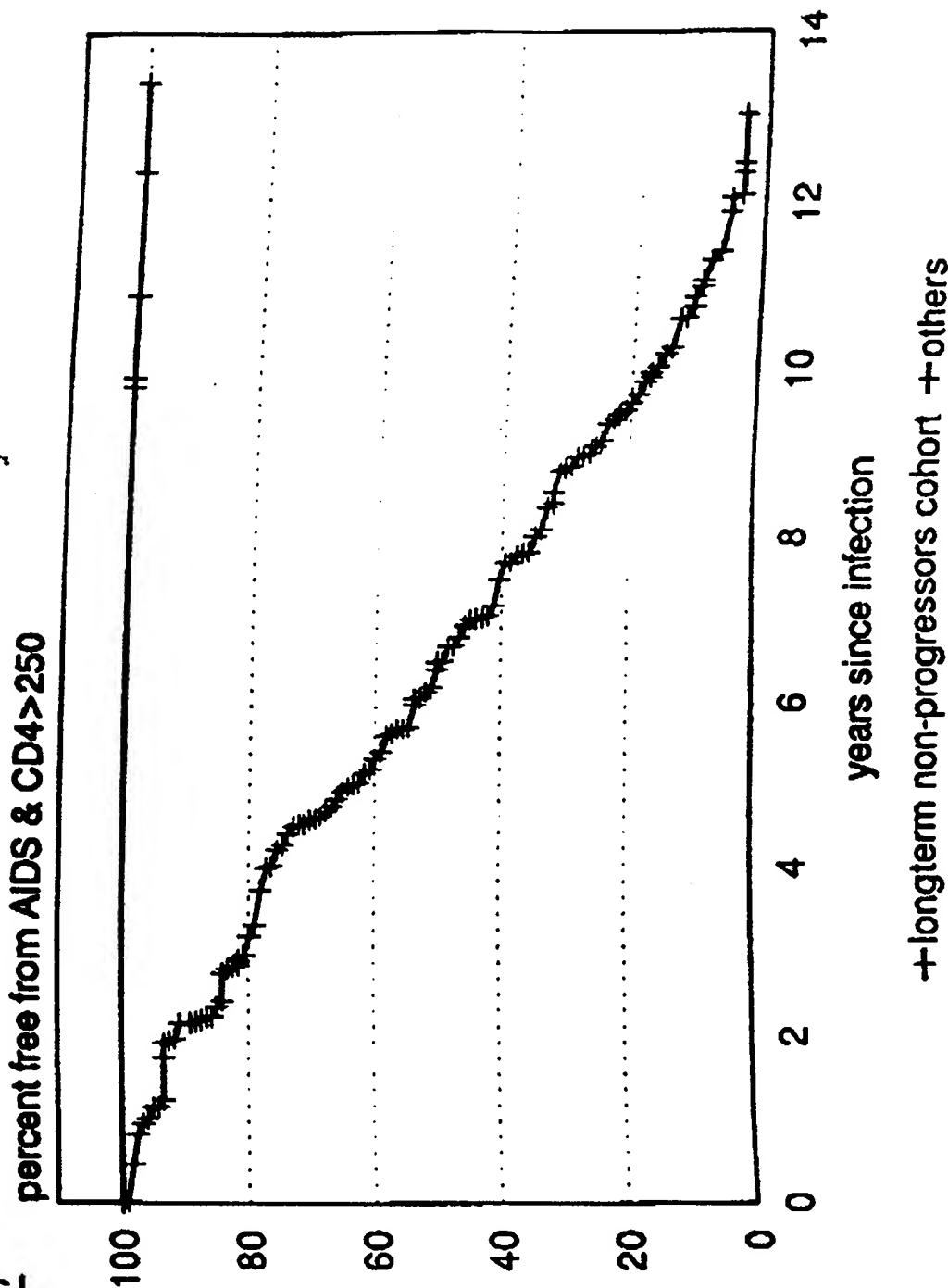
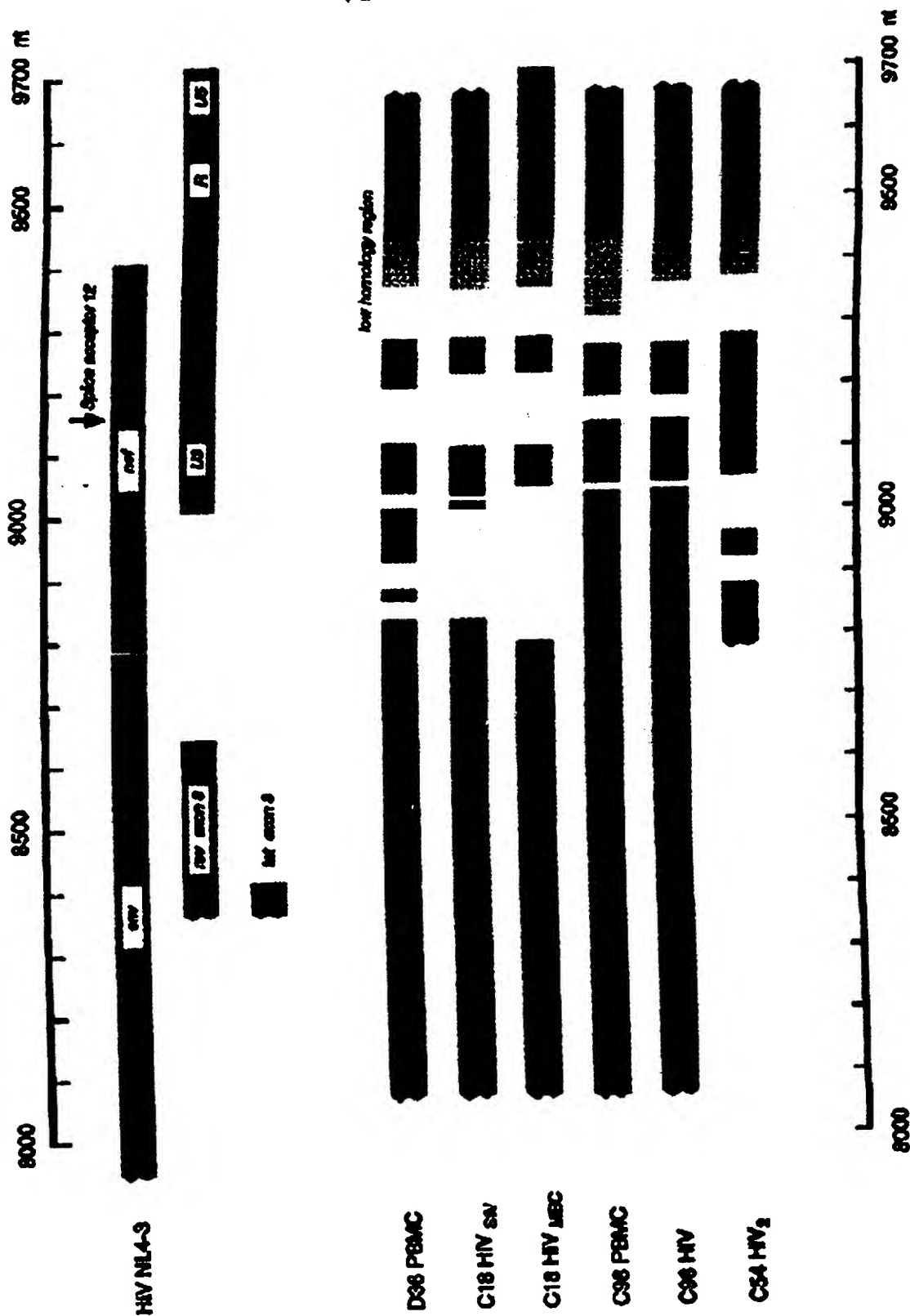


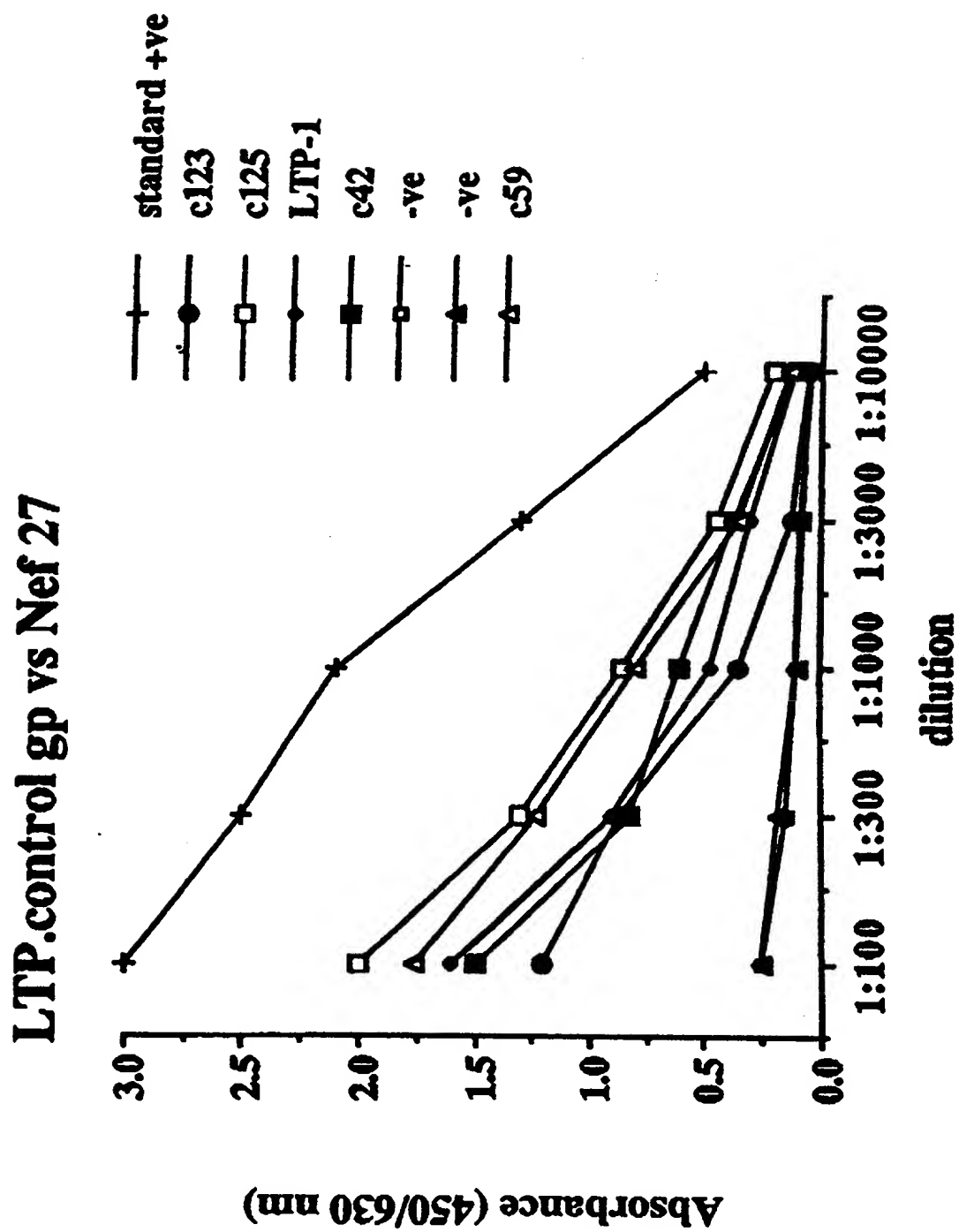
FIGURE 11

45/101



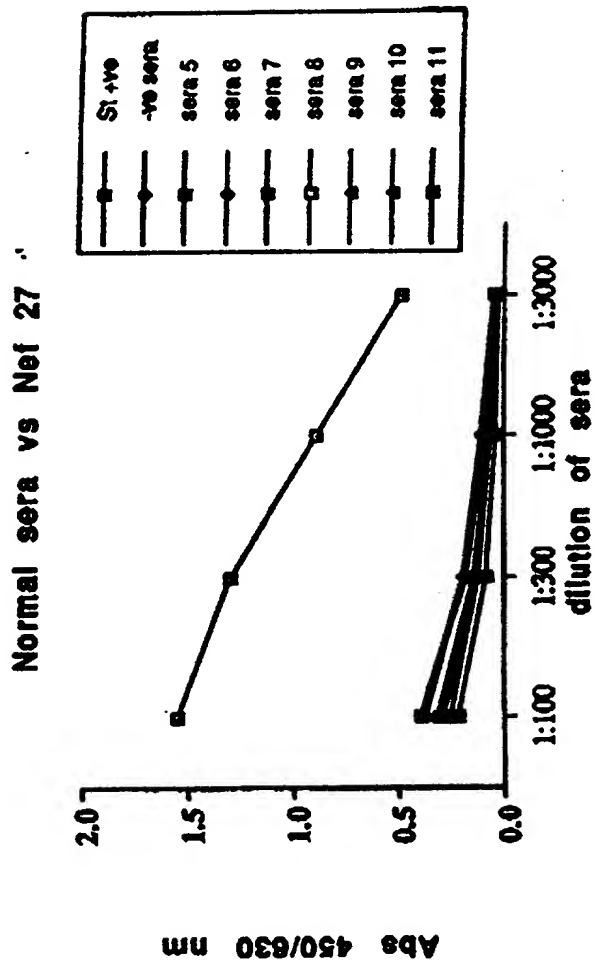
35E060* E6254T60

46/101
FIGURE 12A



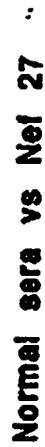
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DATA

47/101
FIGURE 12B(i)



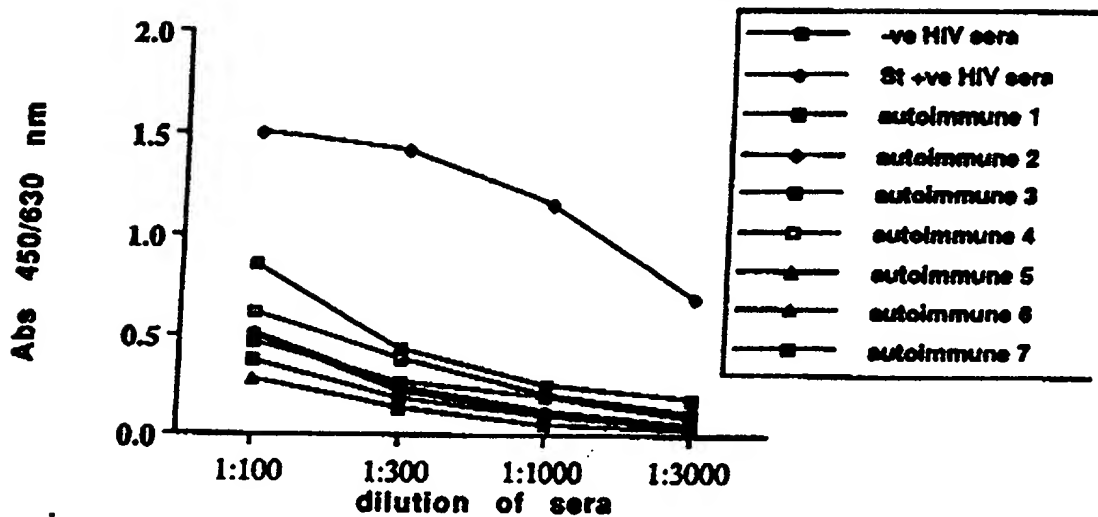
Abstract

25



49/101

Nef 27 vs Autoimmune sera



Autoimmune sera 2 vs Nef 27

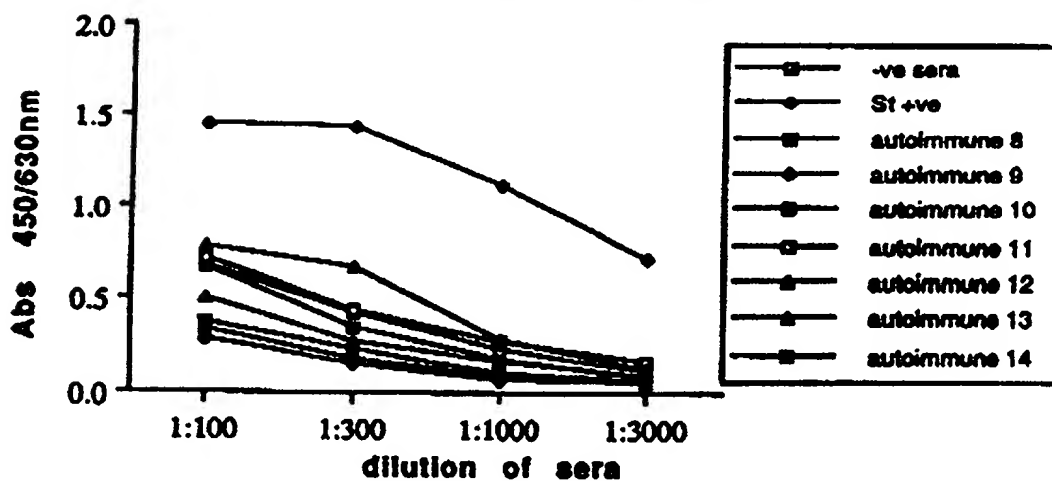
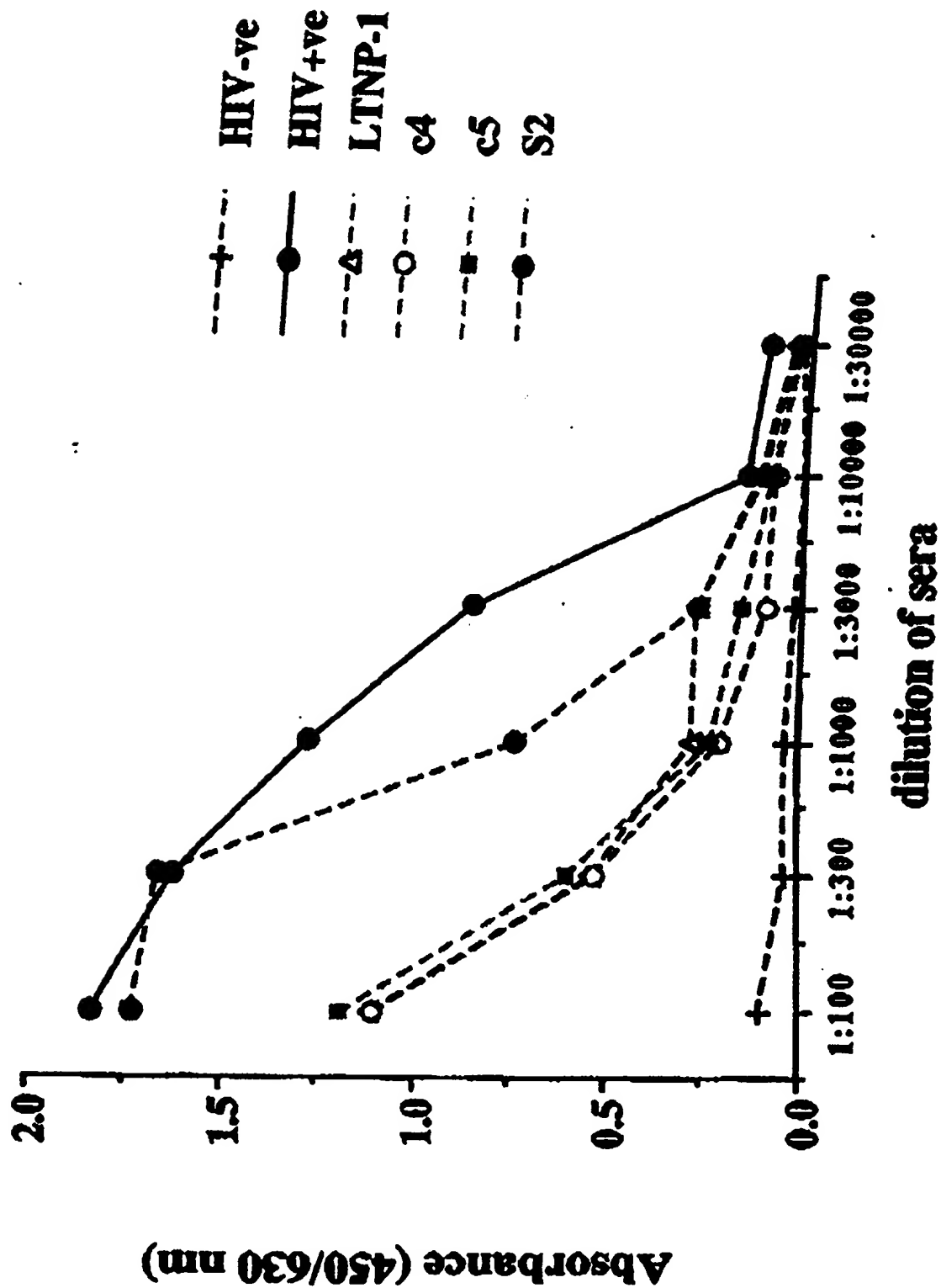


FIGURE 12B(iii)

[illegible]

51/101
FIGURE 12D

Non-progressor sera vs Nef 27

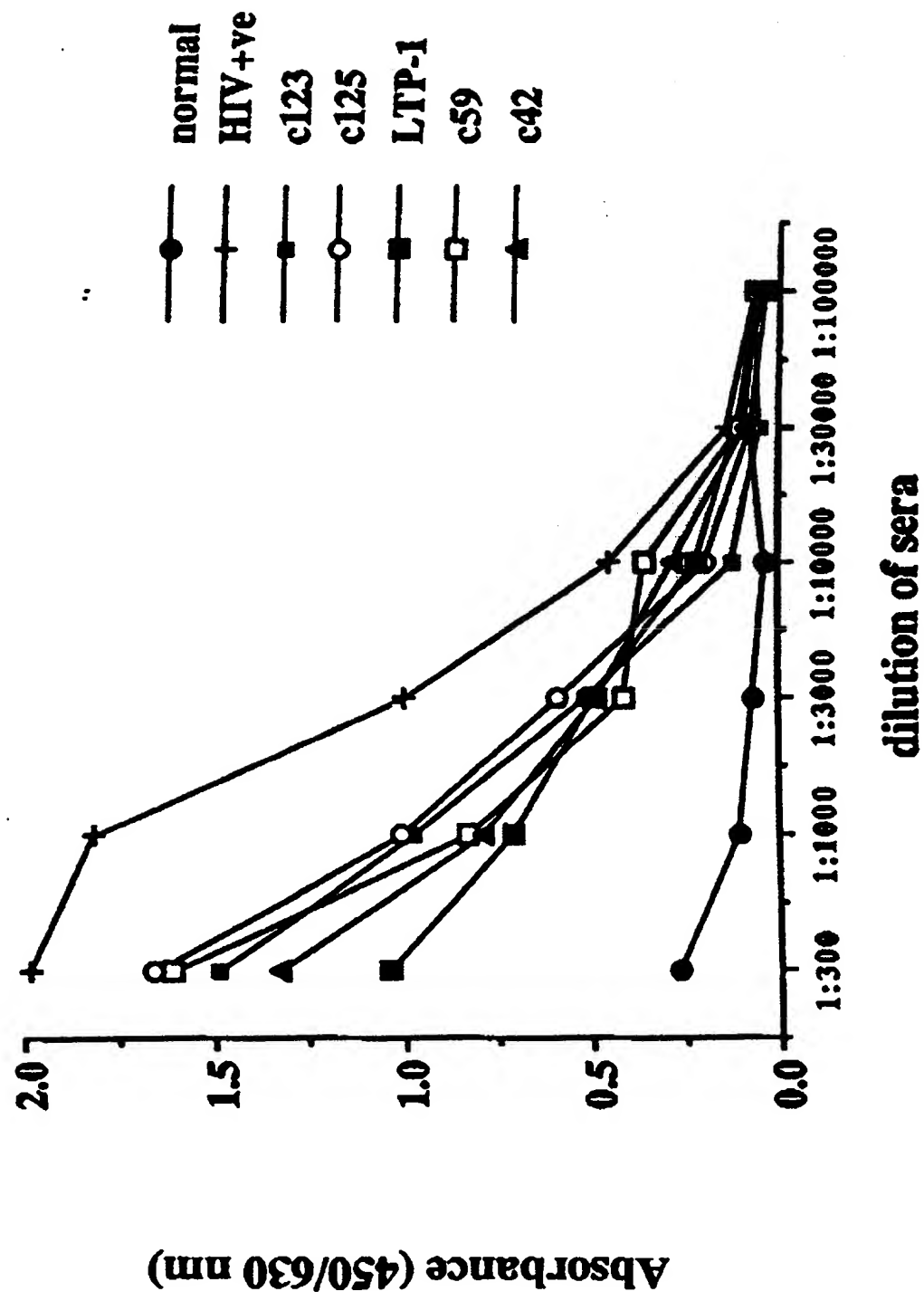


BBE000-EB294T00

52/101

FIGURE 13A(i)

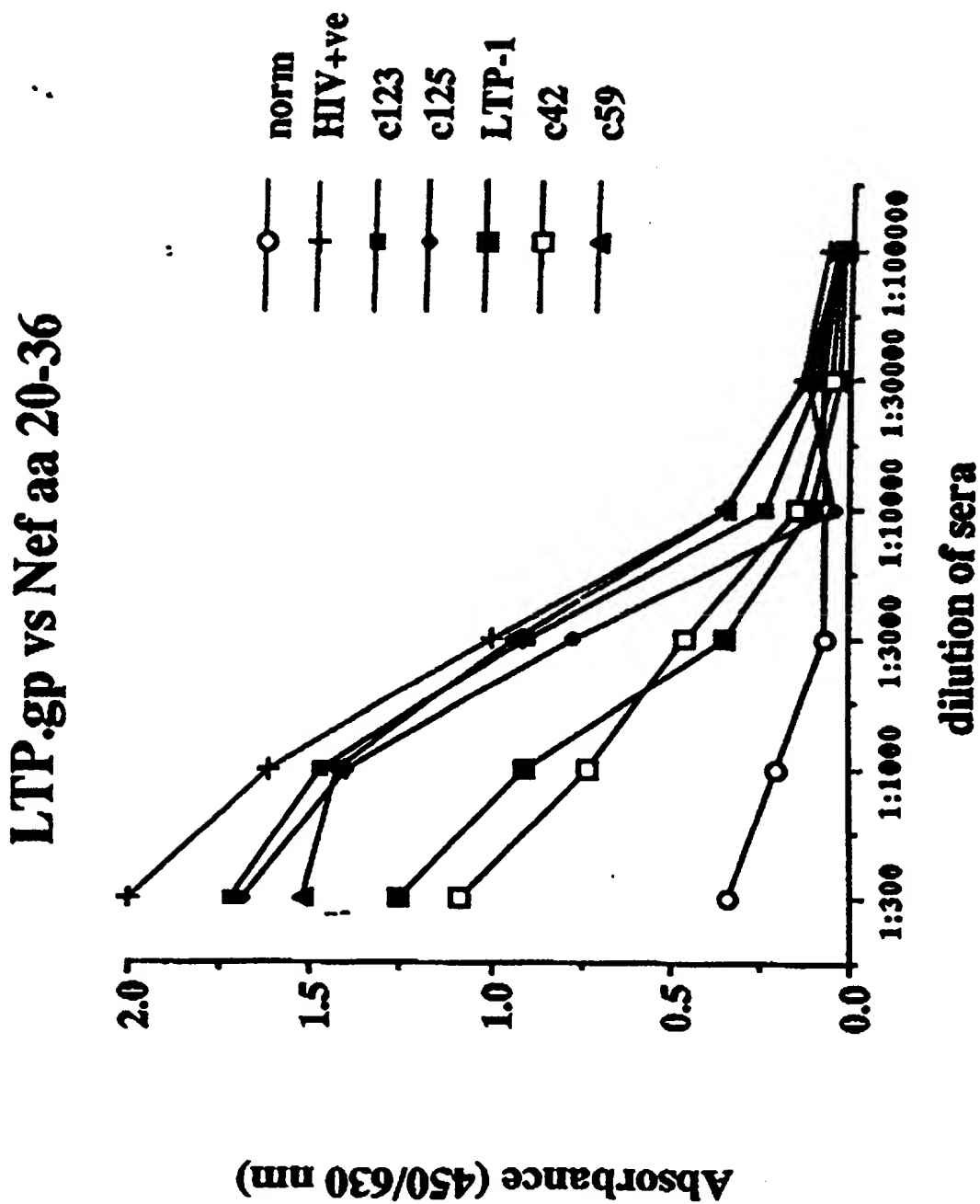
LTP gp.vs Nef aa1-19



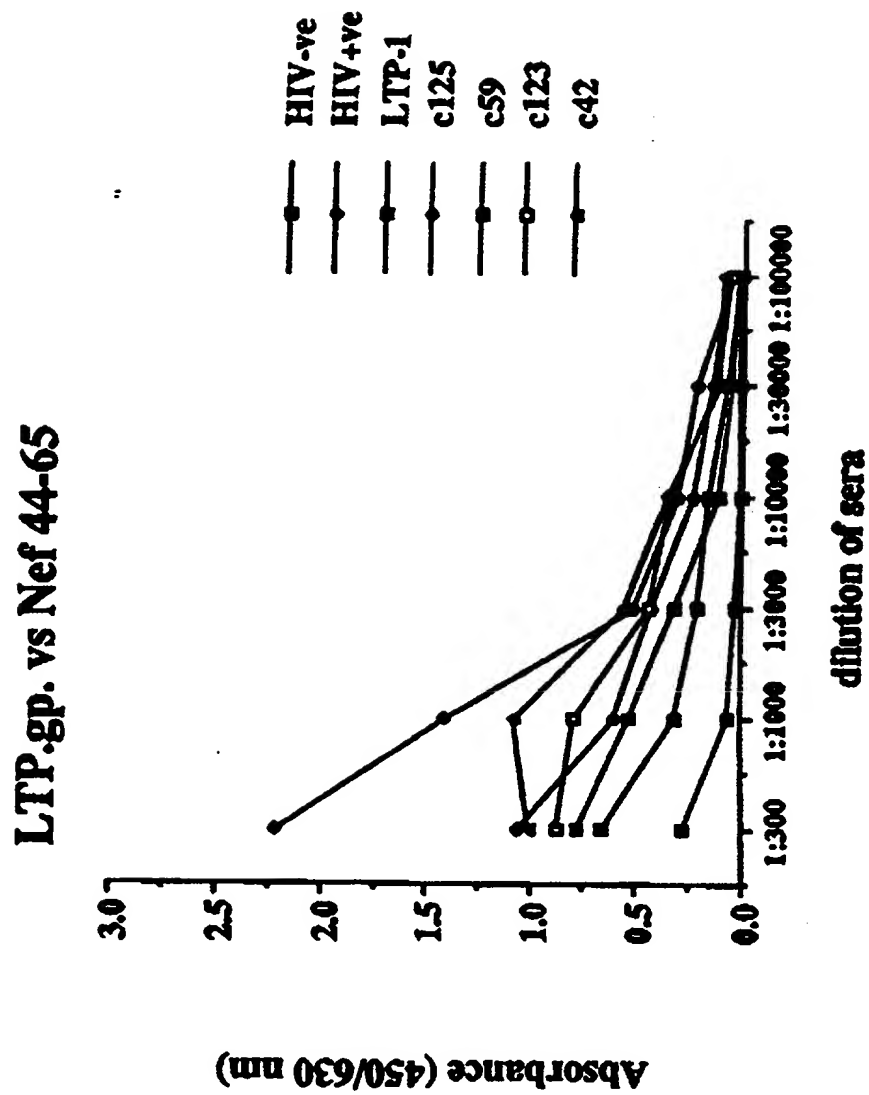
800000-28294160

53/101

FIGURE 13A (ii)

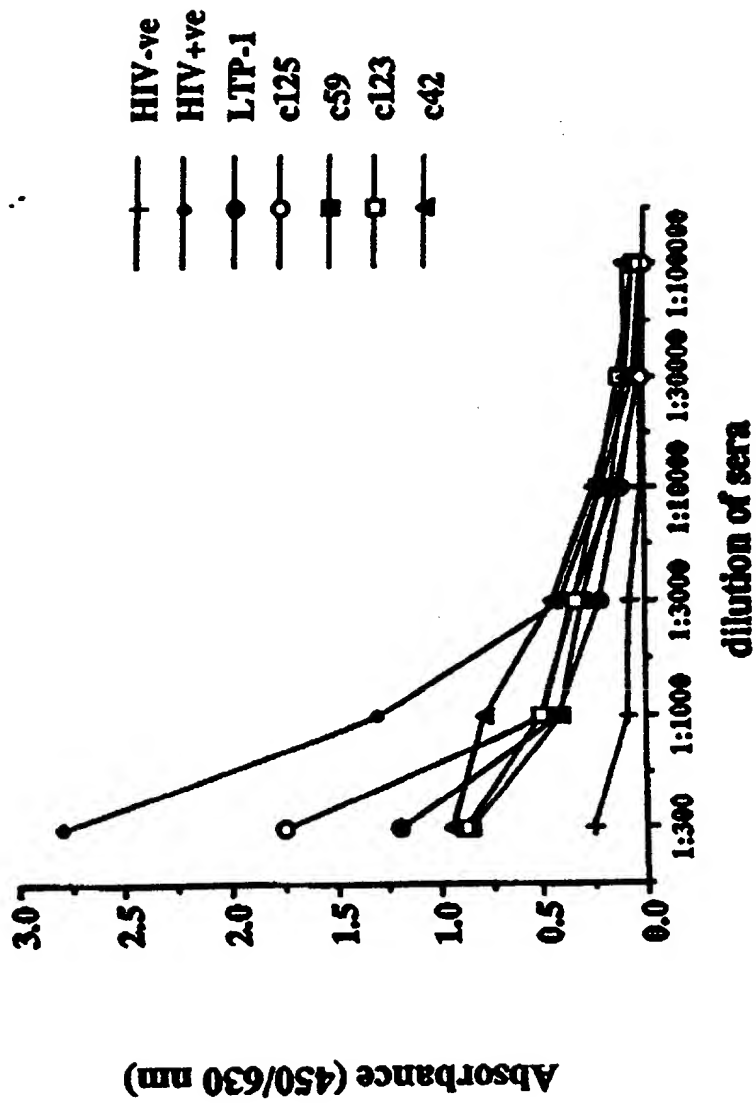


54/101
FIGURE 13A (iii)



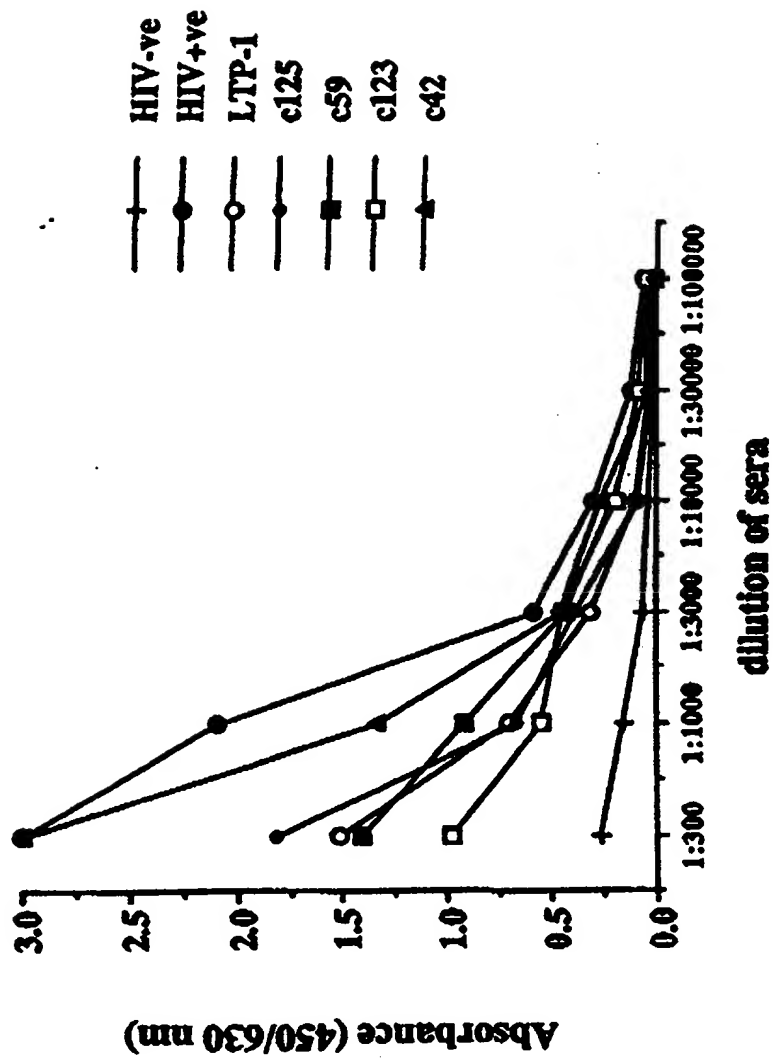
55/101
FIGURE 13A (iv)

LTP.gp. vs Nef aa 72-83

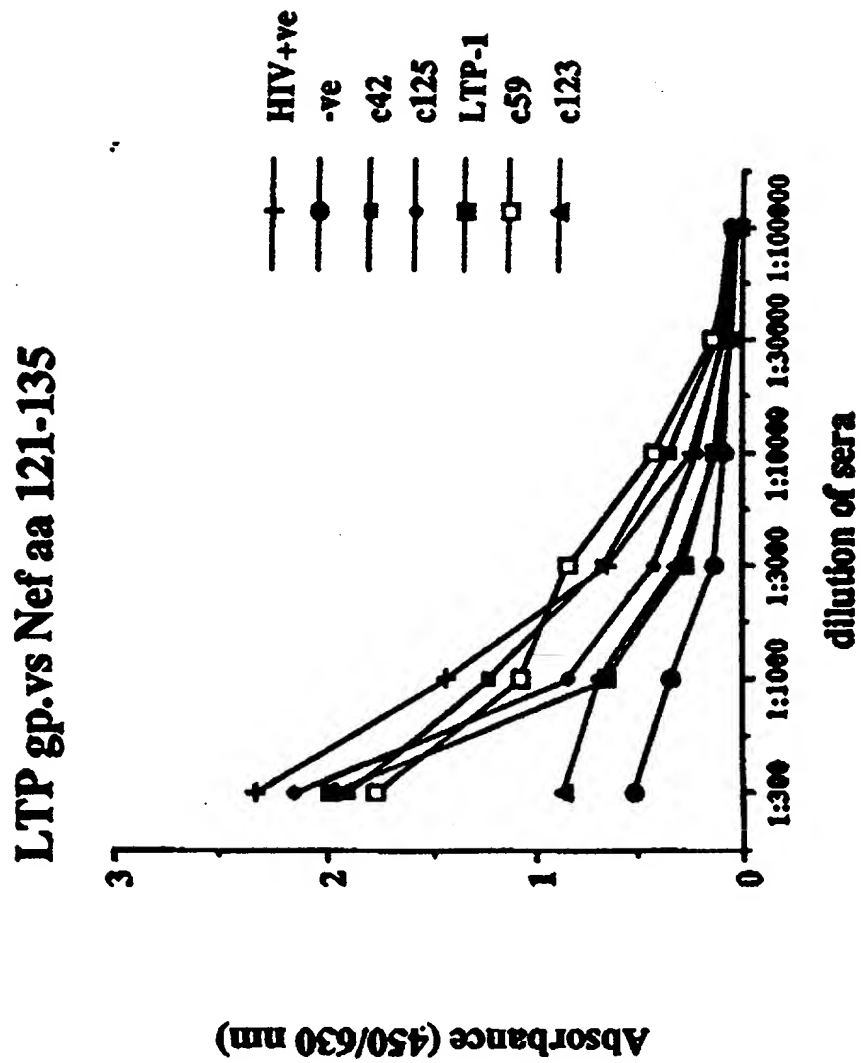


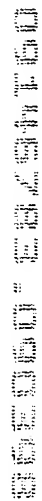
56/101
FIGURE 13A (v)

LTP.gp. vs Nef aa 89-97



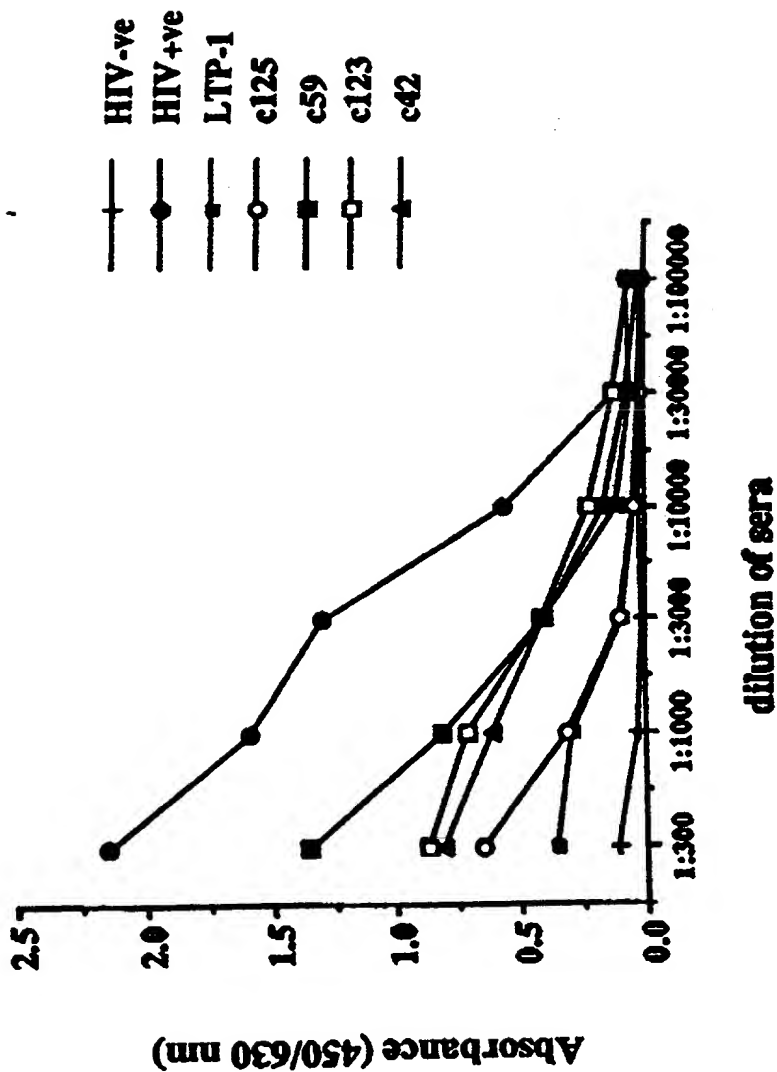
88/101
FIGURE 13A (ii)



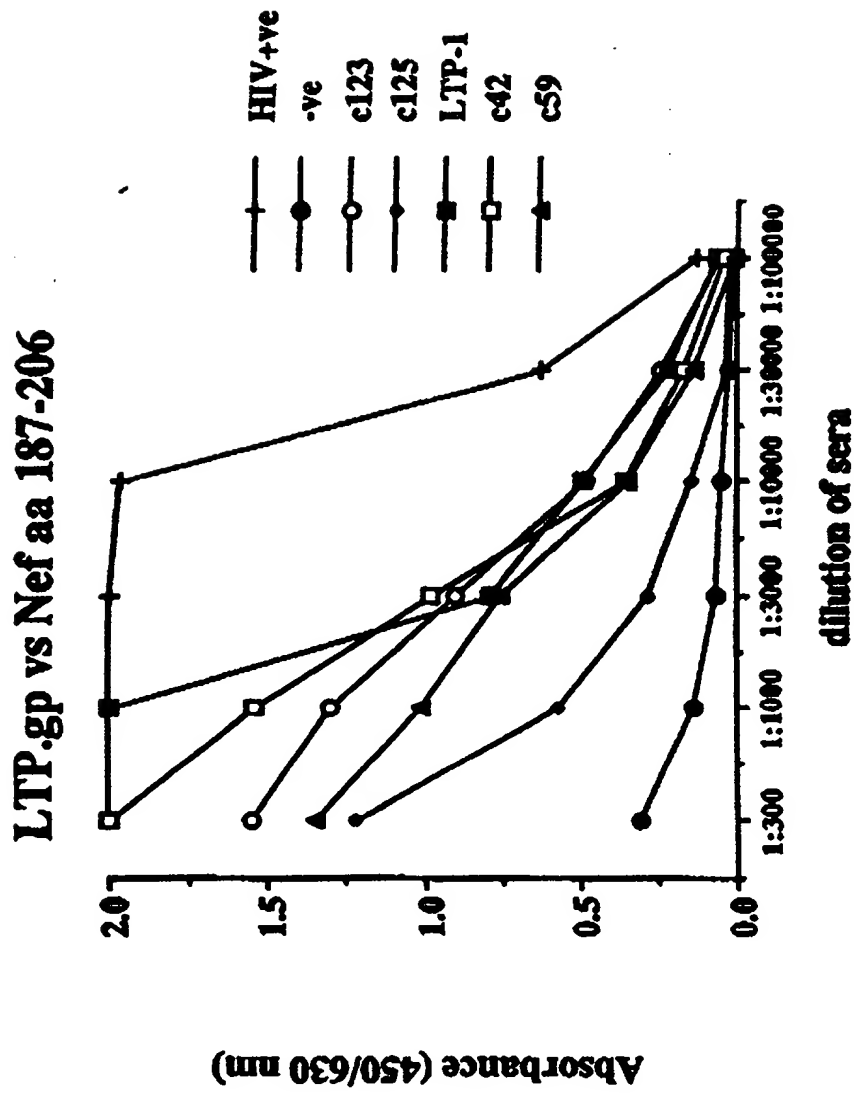
[illegible][illegible]

60/101
FIGURE 13A (ix)

LTP.gp. vs Nef 164-186



61/101
FIGURE 13A(x)



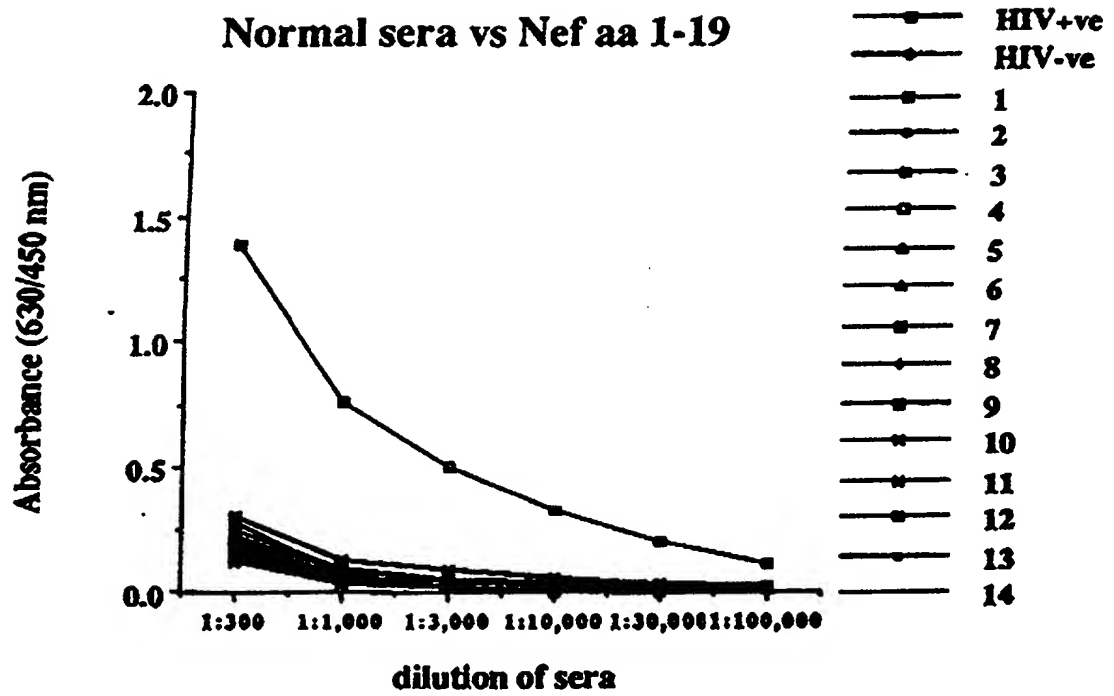
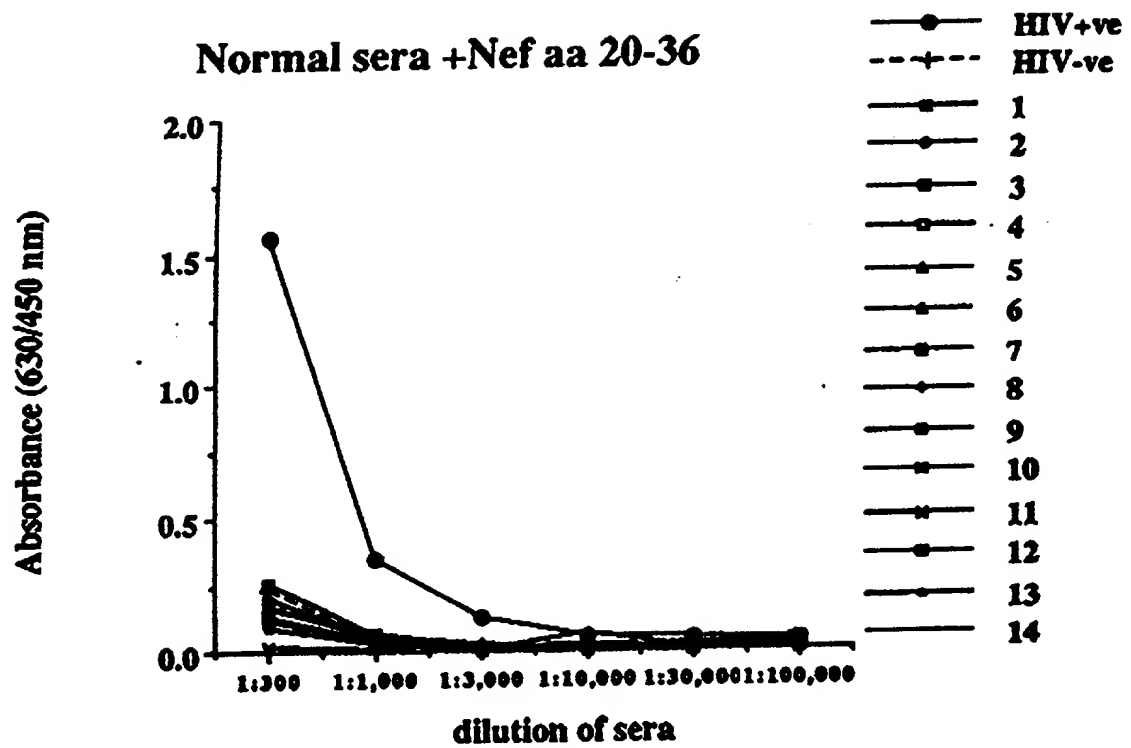
[illegible]

FIGURE 13B (i)(ii) 63/101



64/101
FIGURE 13B (i) (ii)

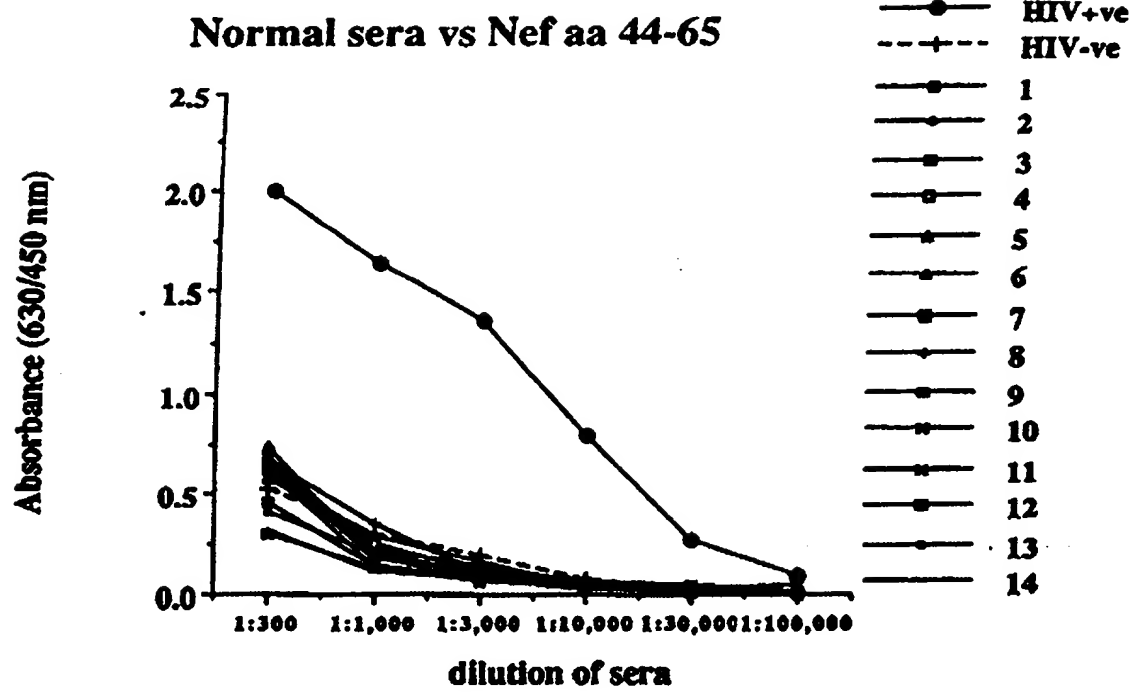
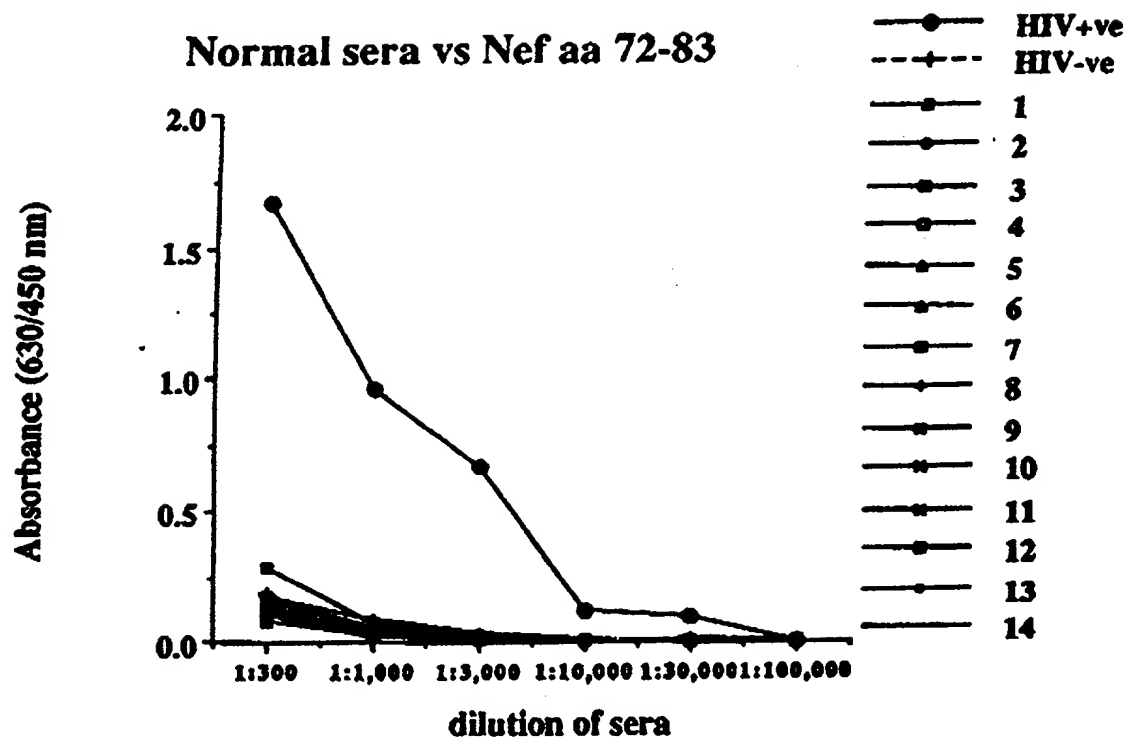


FIGURE 13B (i) (iv)



THE GARDEN

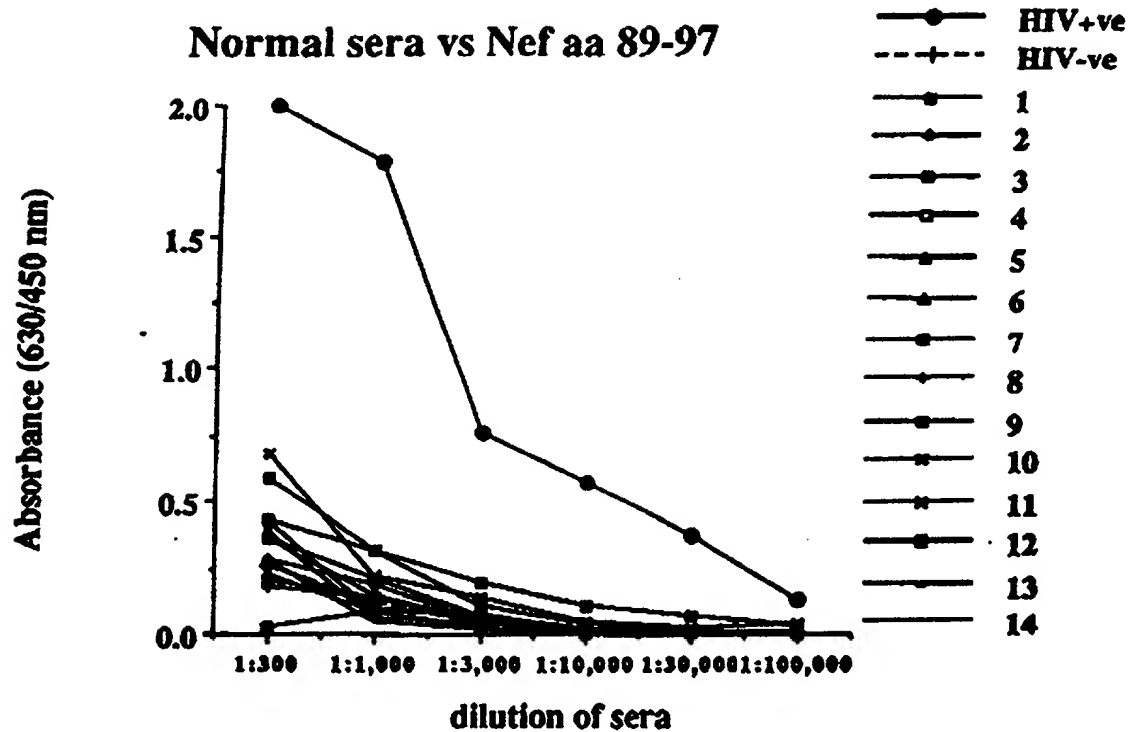
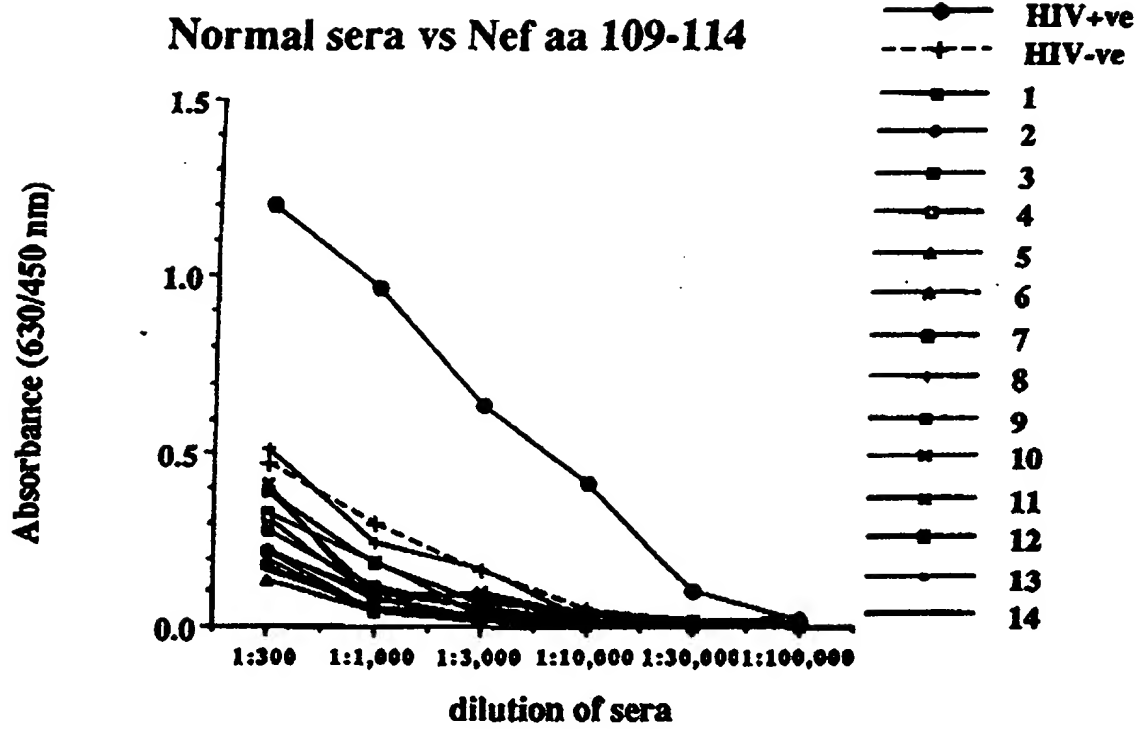
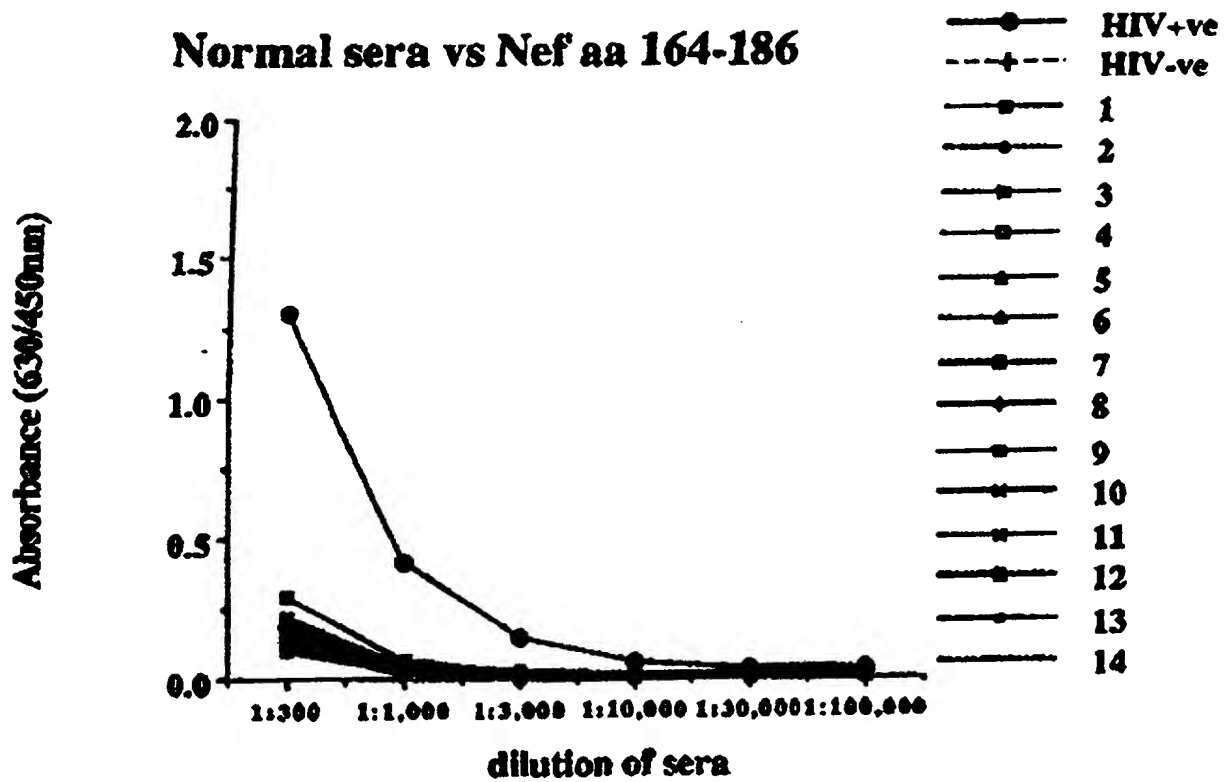


FIGURE 13B (i) (vi) 67/101



[illegible]

FIGURE 13 B (i) (vii)



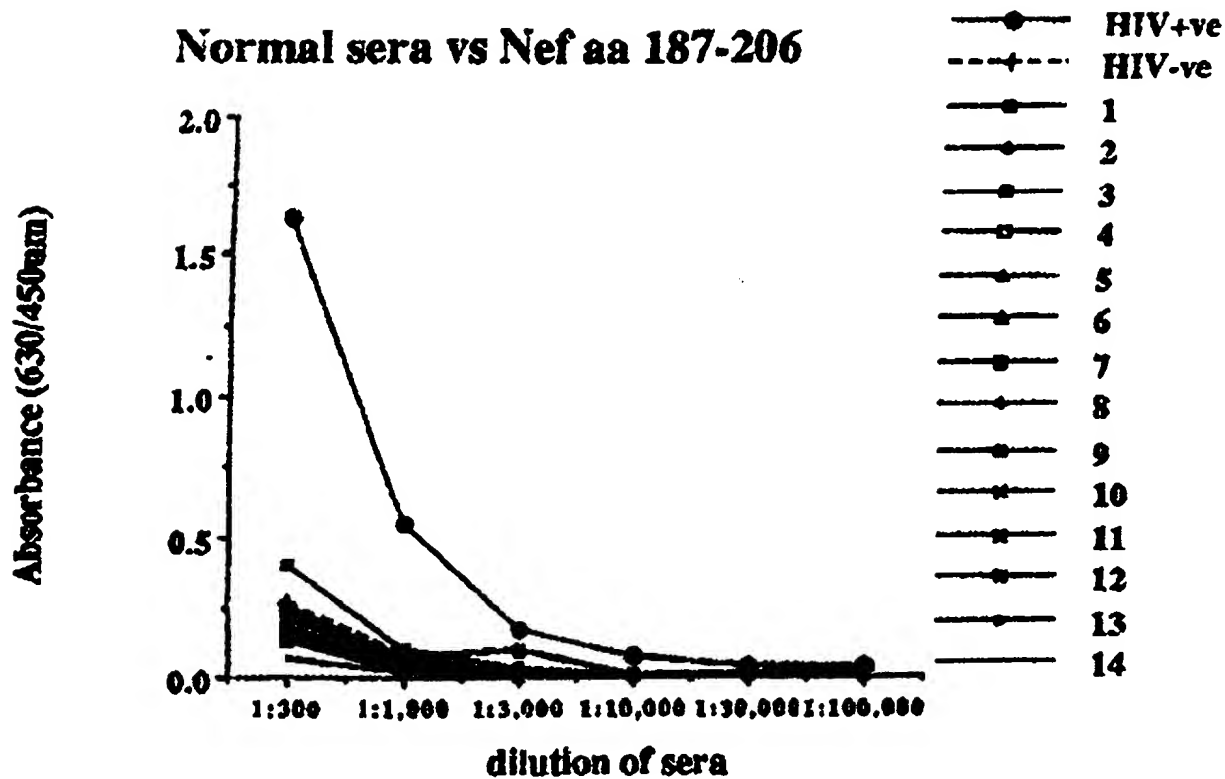
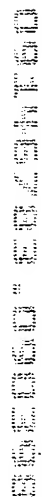
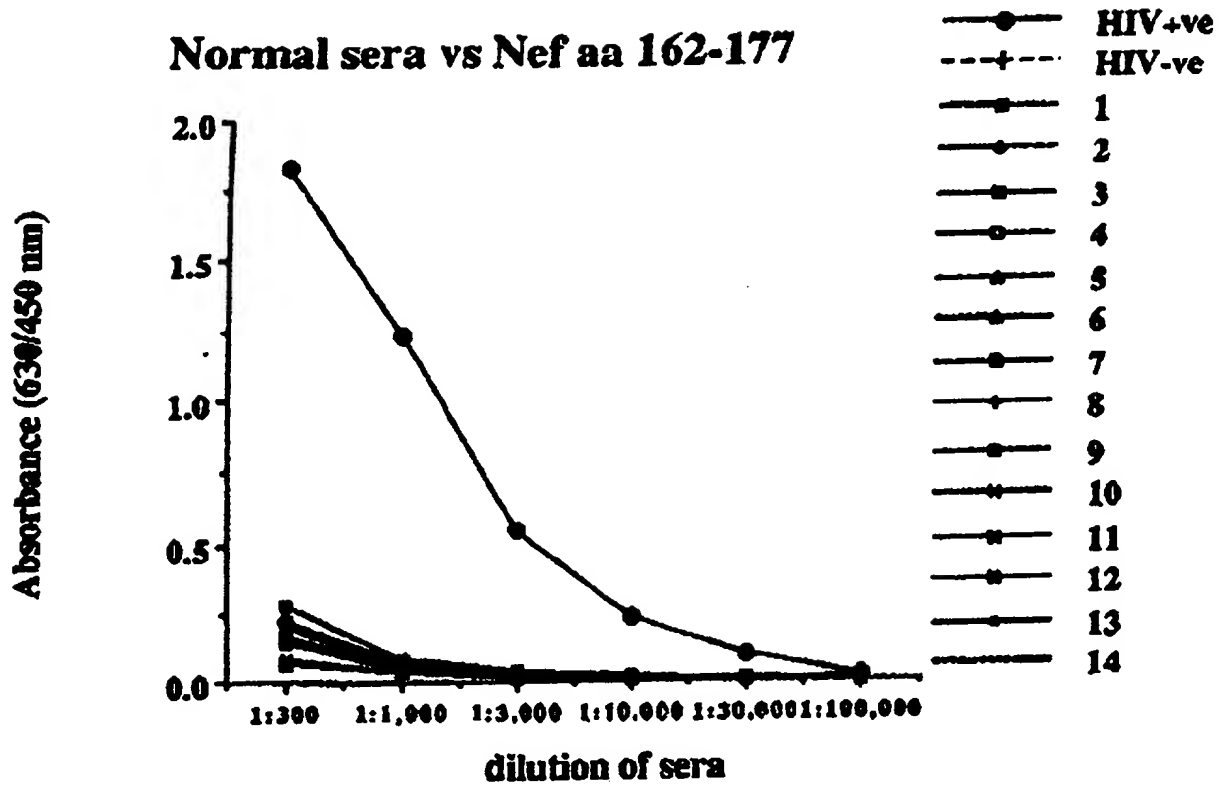
[illegible]

FIGURE 13B (i) (ix) ^{70/101}



71/101

FIGURE 13 B (i) (x)



1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
 24. **Figure 16**
 25. **Figure 17**
 26. **Figure 18**
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 28. **Figure 20**
 29. **Figure 21**
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 207. **Figure 199**
 208. **Figure 200**
 209. **Figure 201**
 210. **Figure 202**
 211. **Figure 203**
 212. **Figure 204**
 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

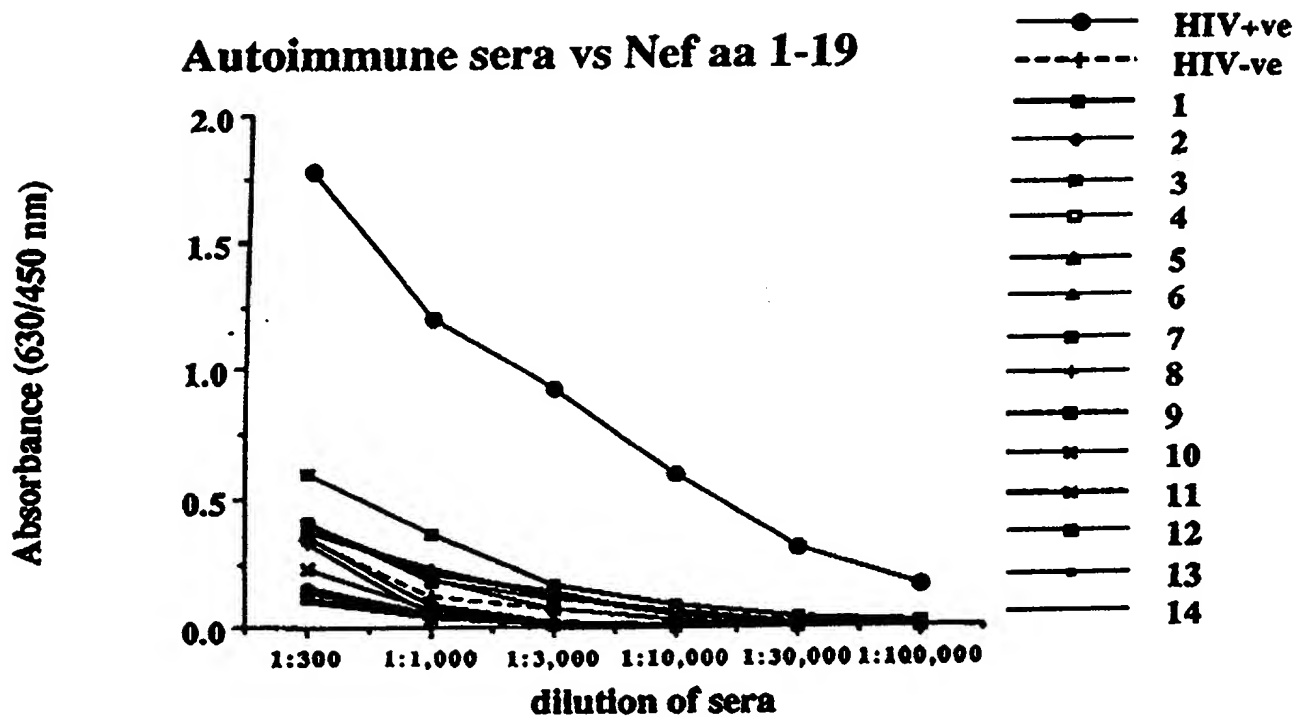
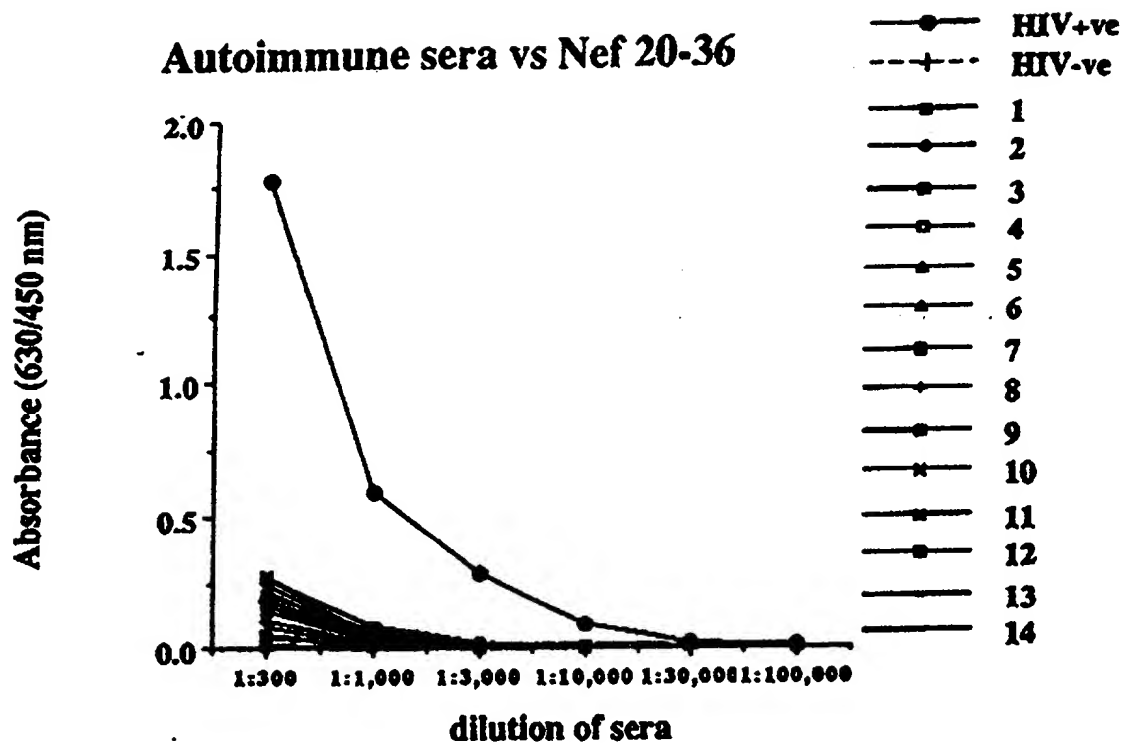


FIGURE 13 B (ii) (i) ^{73/101}



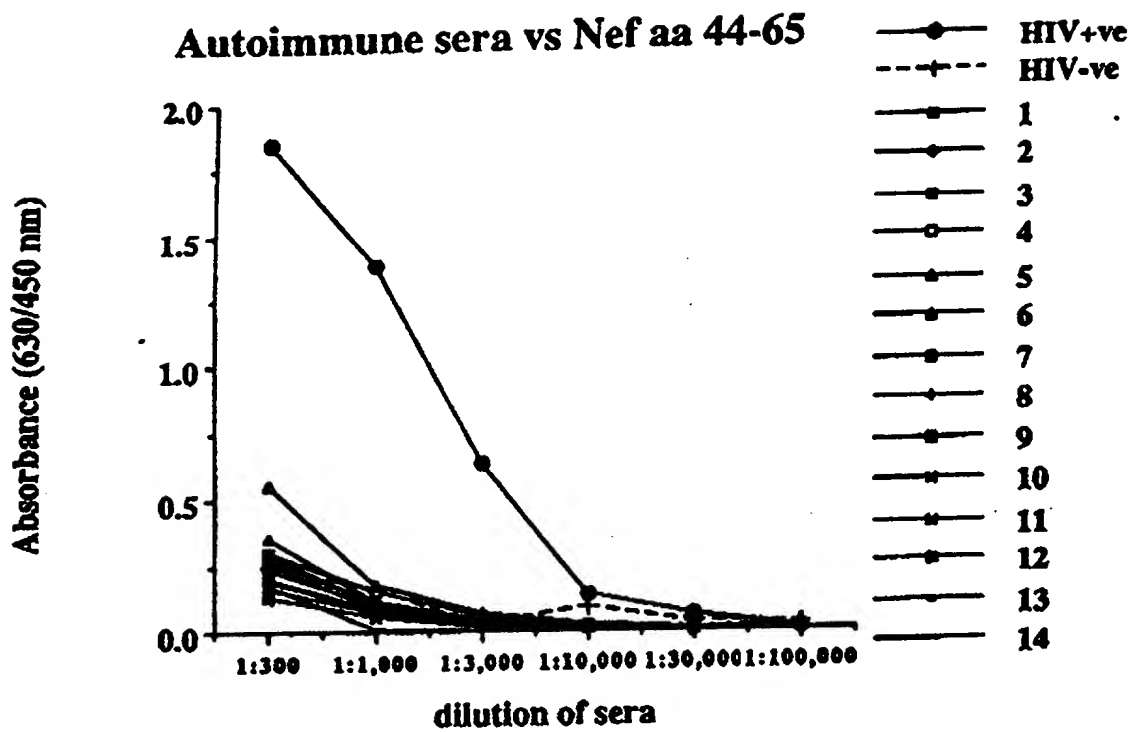
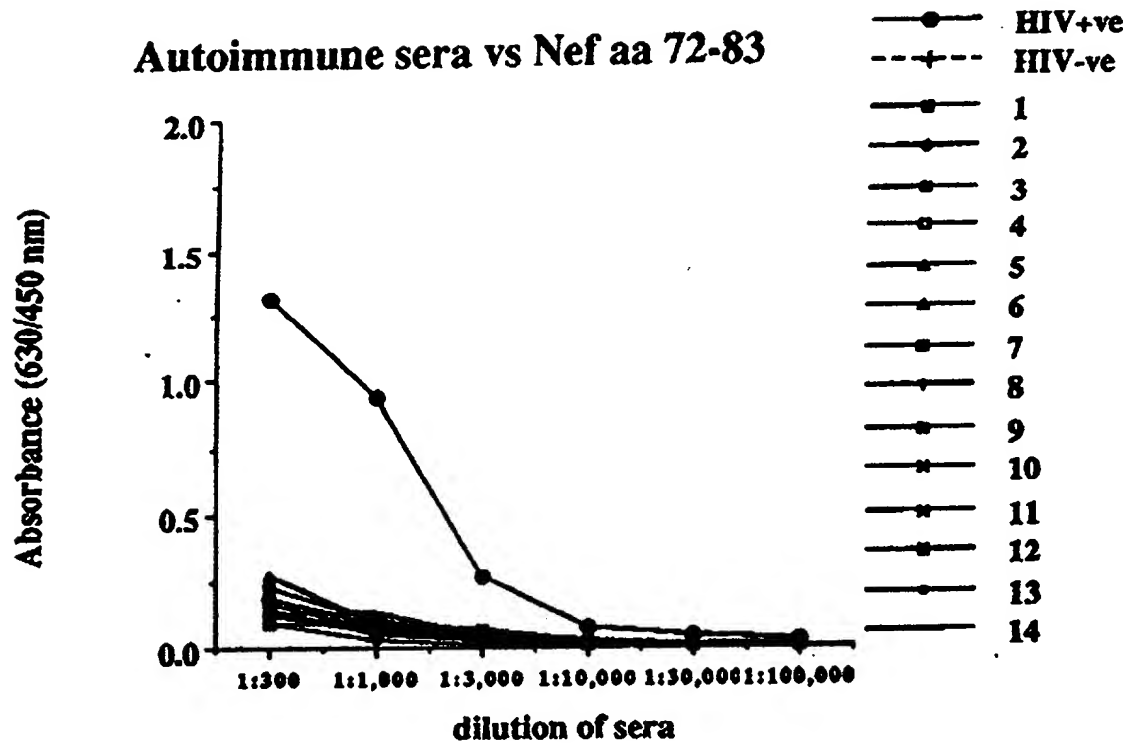
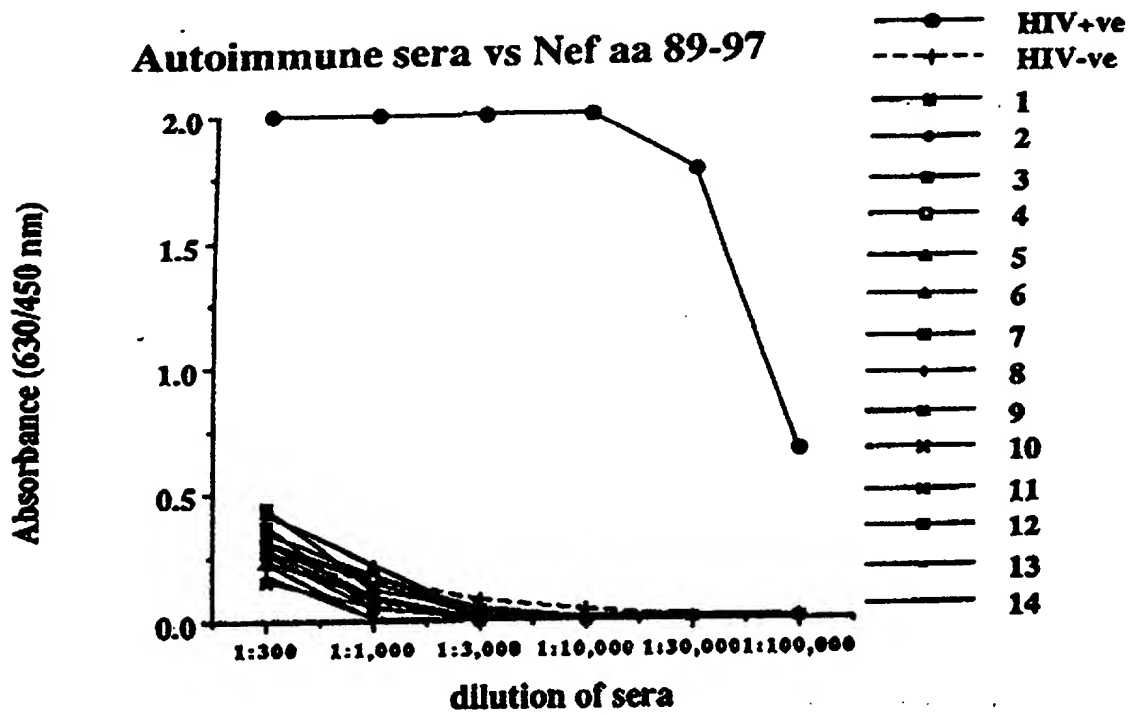
[illegible]

FIGURE 13B (ii) (iv) 75/101

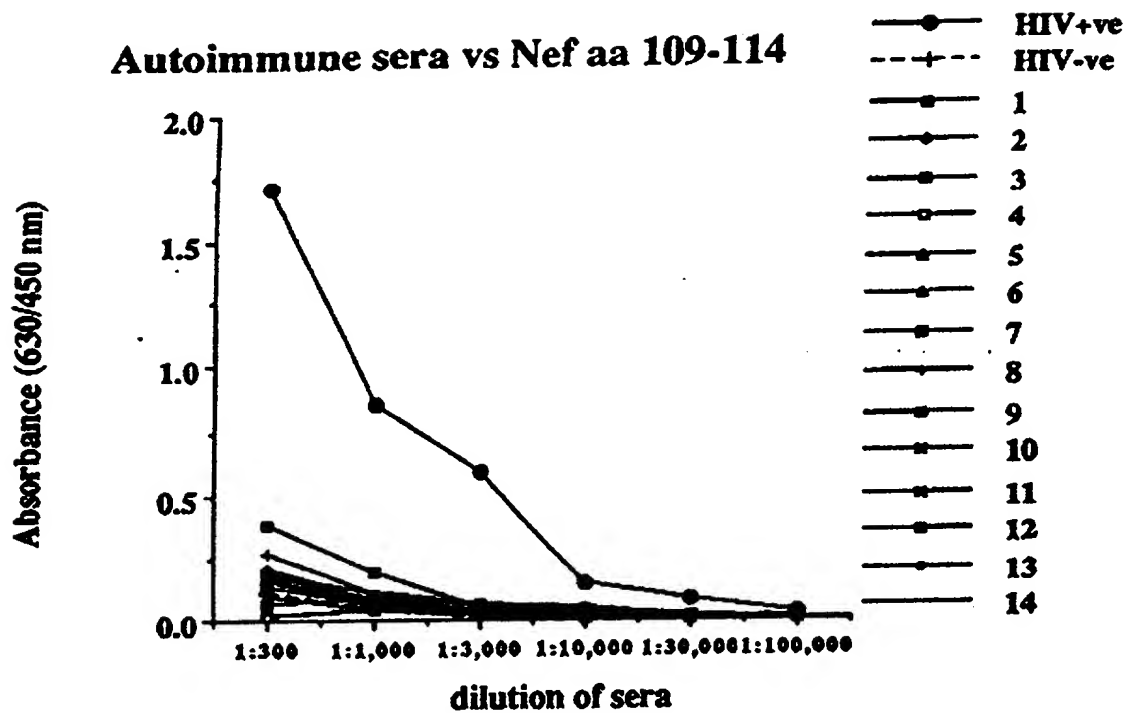


76/101

FIGURE 13(ii) (v)



77/101



78/101

FIGURE 13 B (ii) (vii)

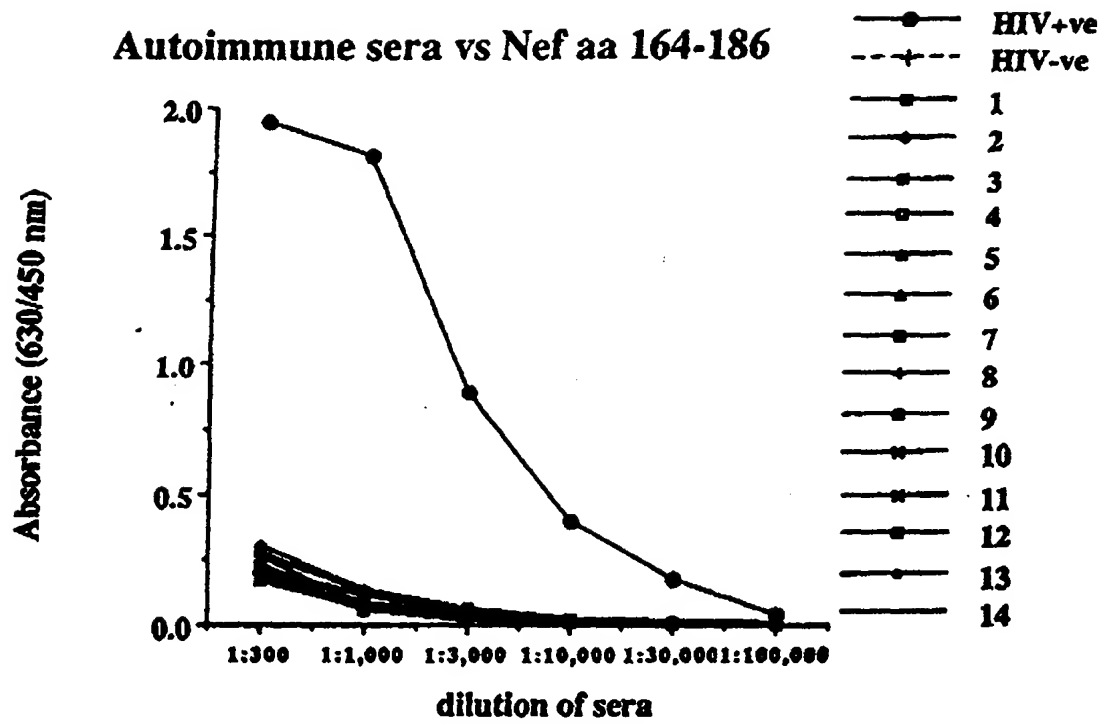
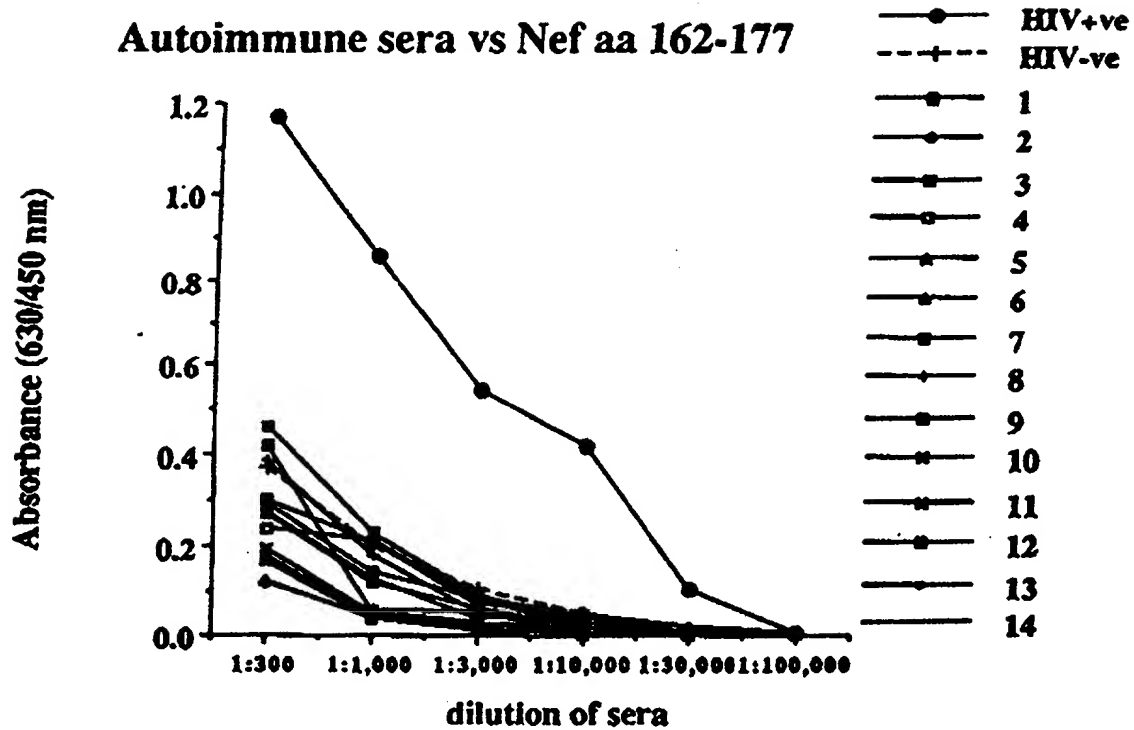
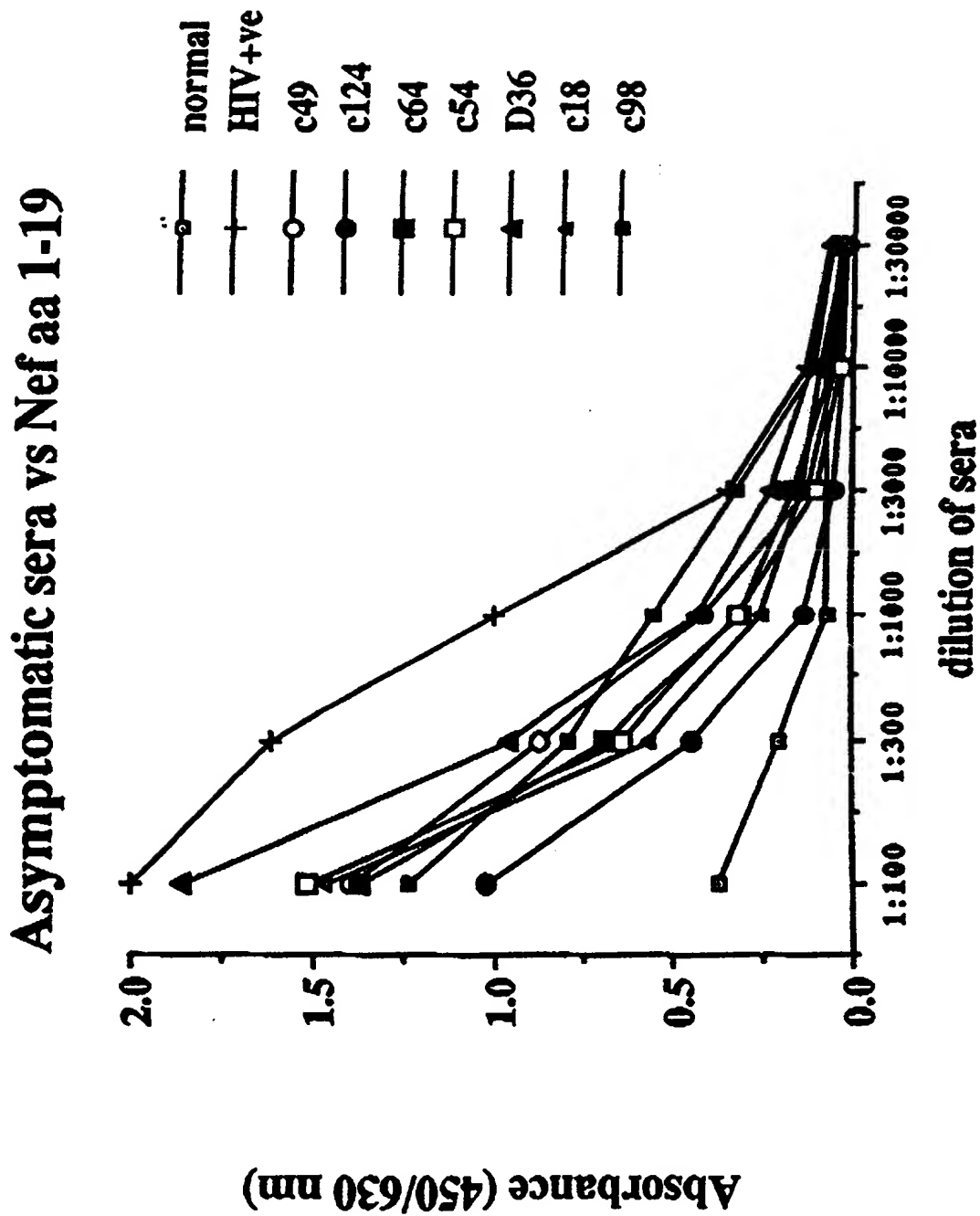


FIGURE 13 B (1) (x) 81/101



82/101

FIGURE 13C (i)



Asymptomatic sera vs Nef aa20-36

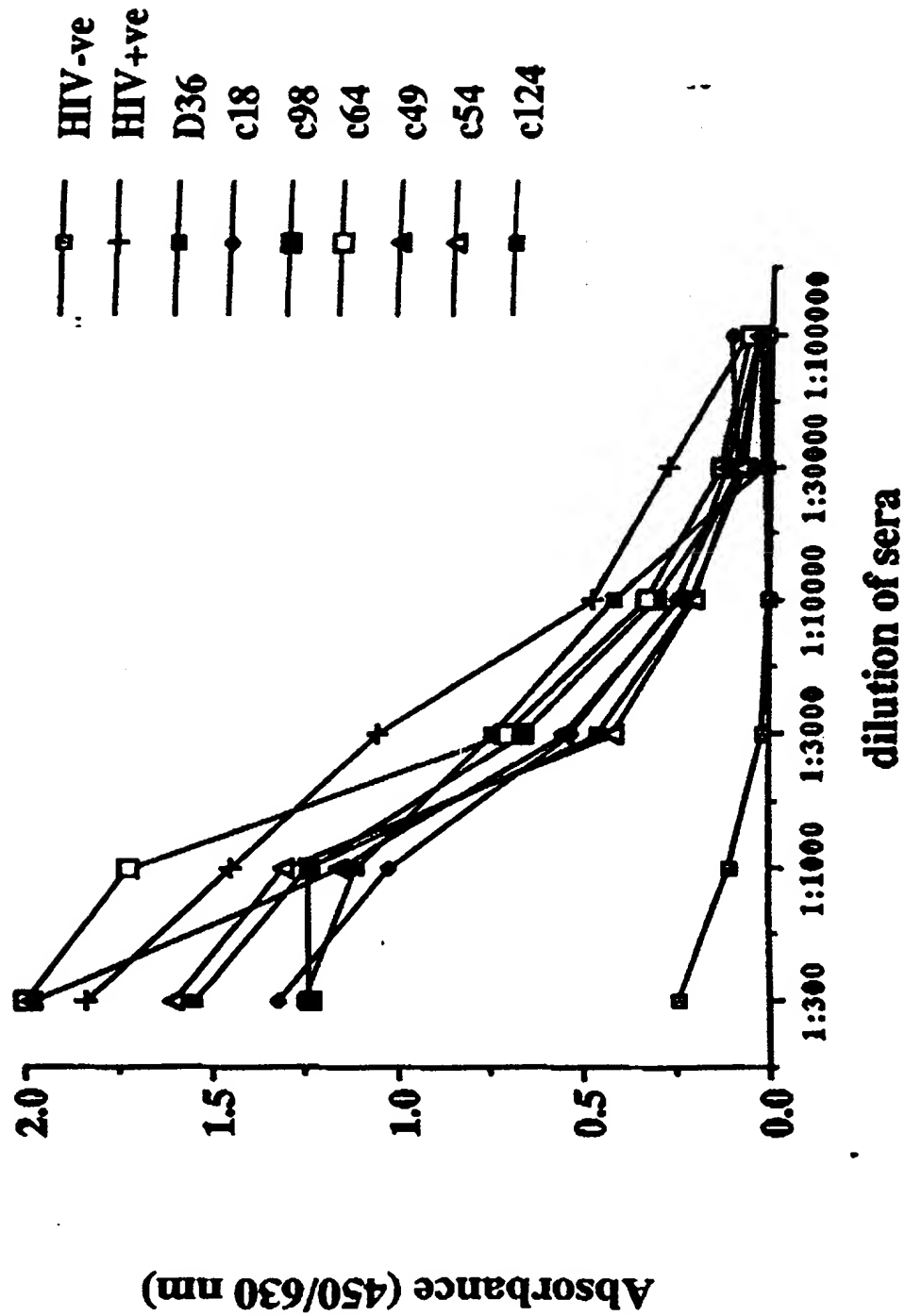
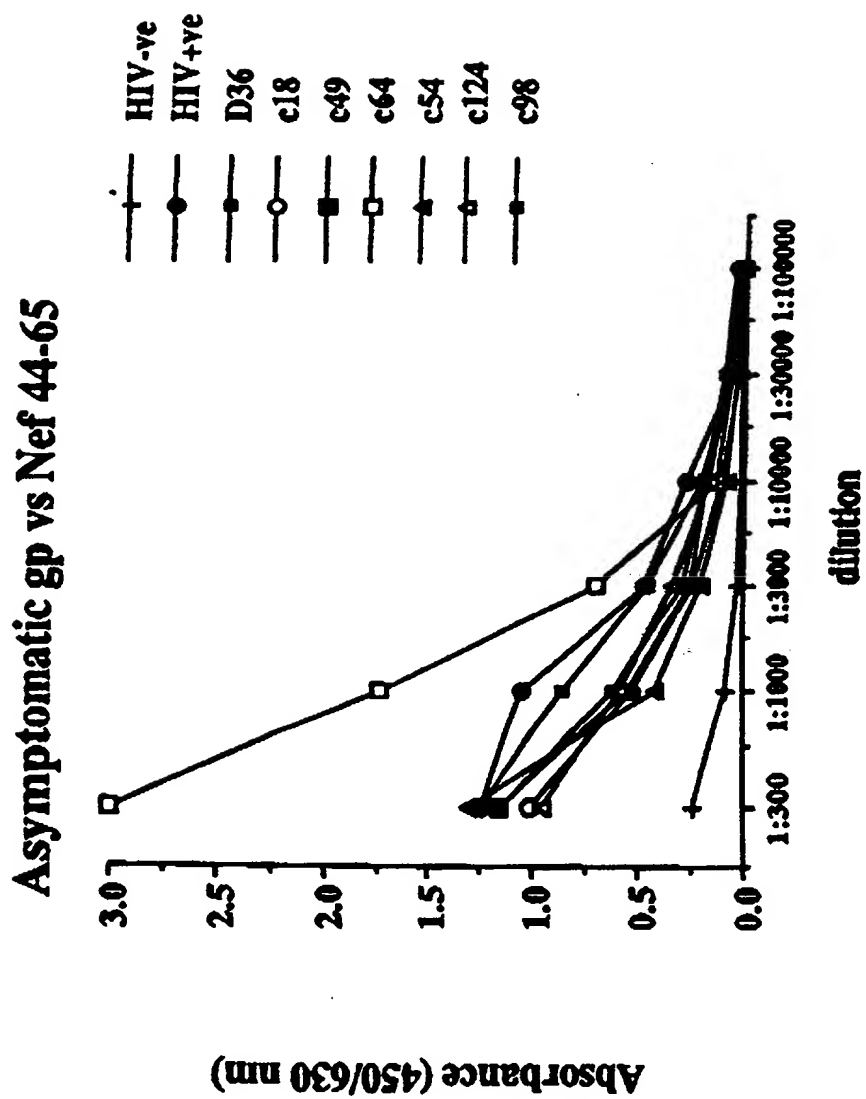


FIGURE 13C (iii)



85/101

FIGURE 13C (iv)

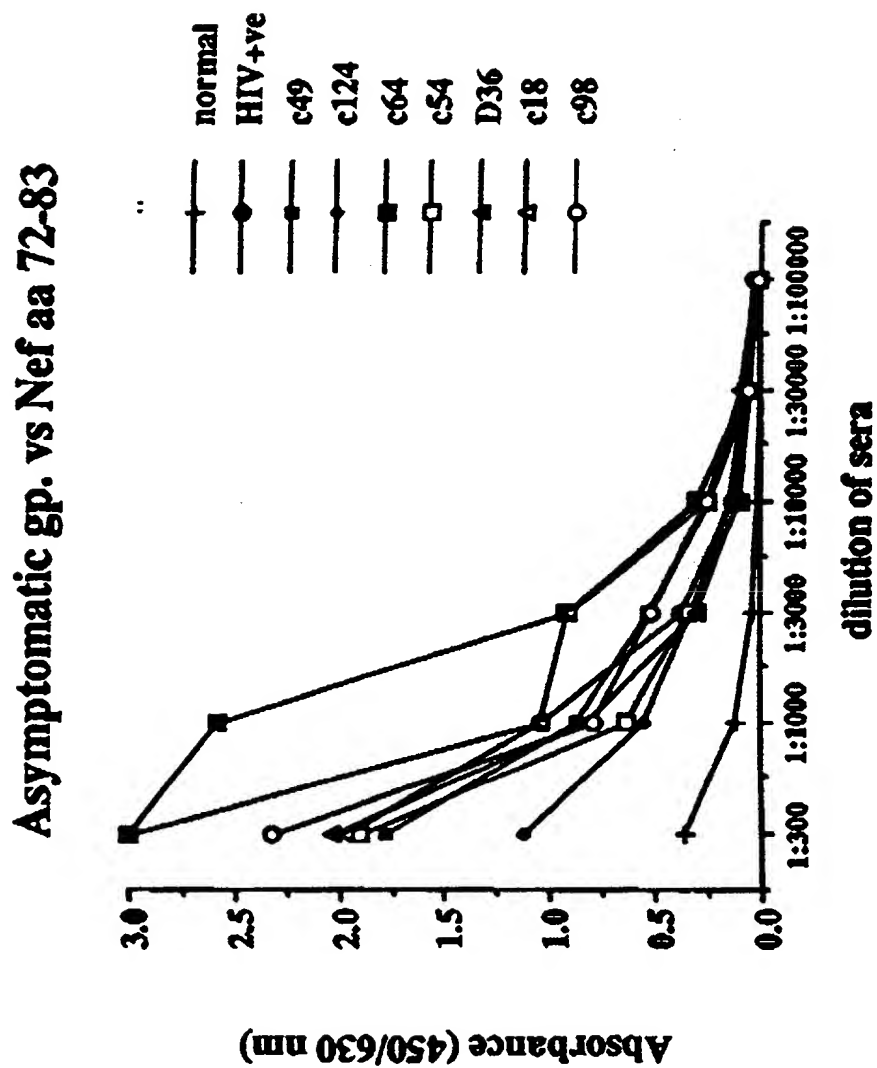
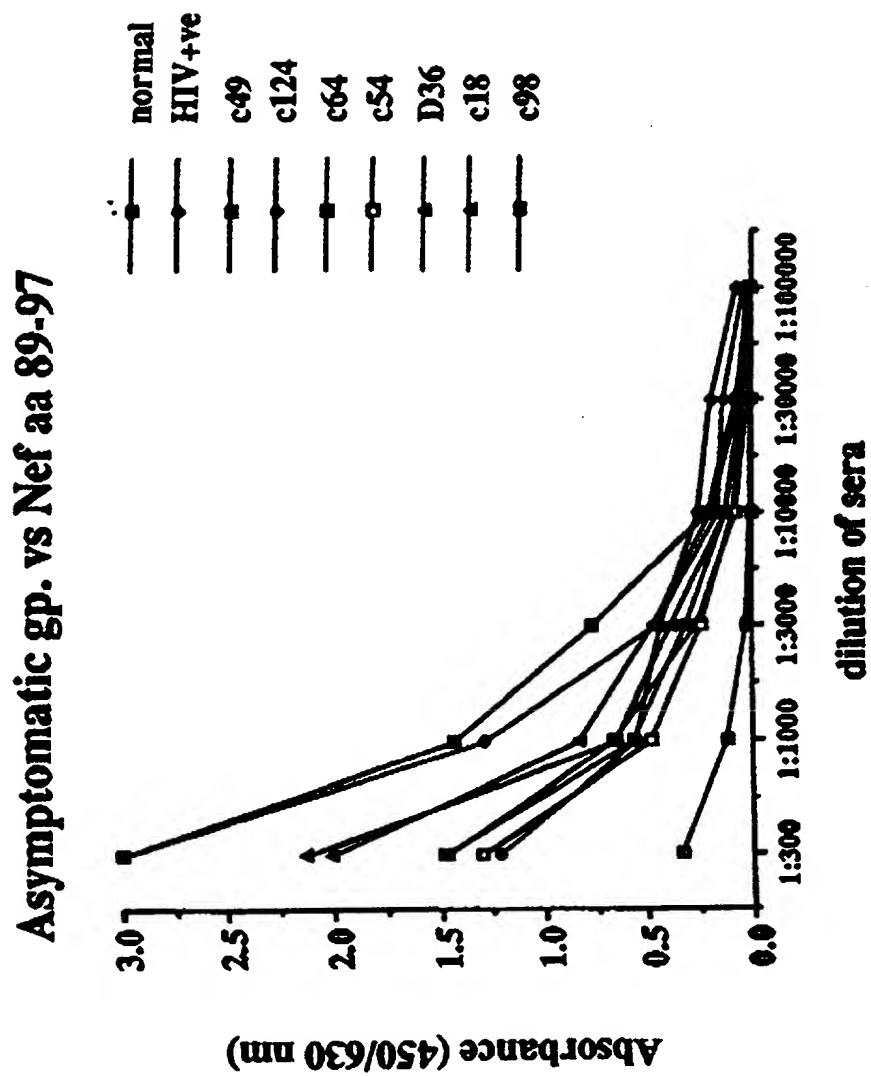


FIGURE 13C (v)



87/101

FIGURE 13C (H)

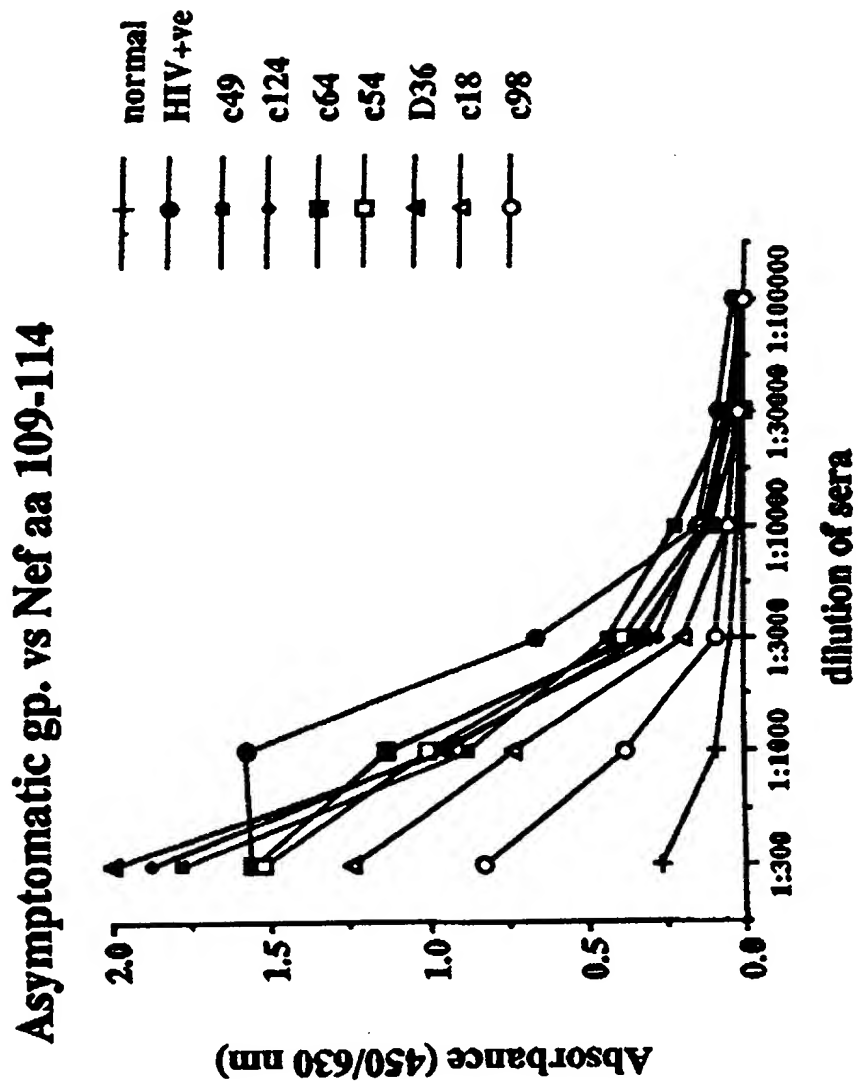
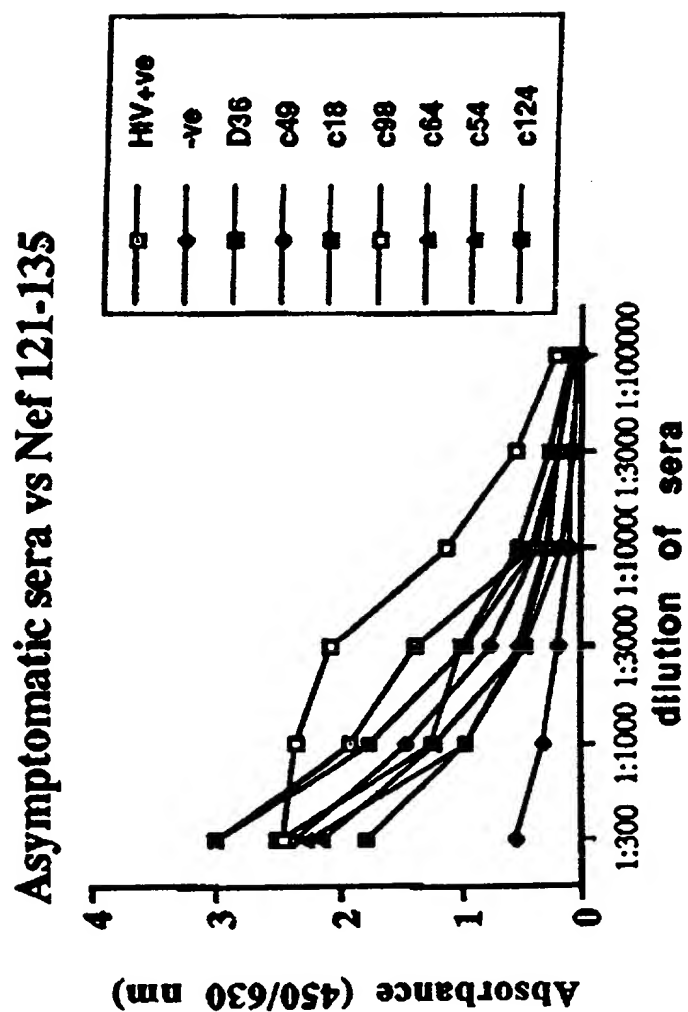
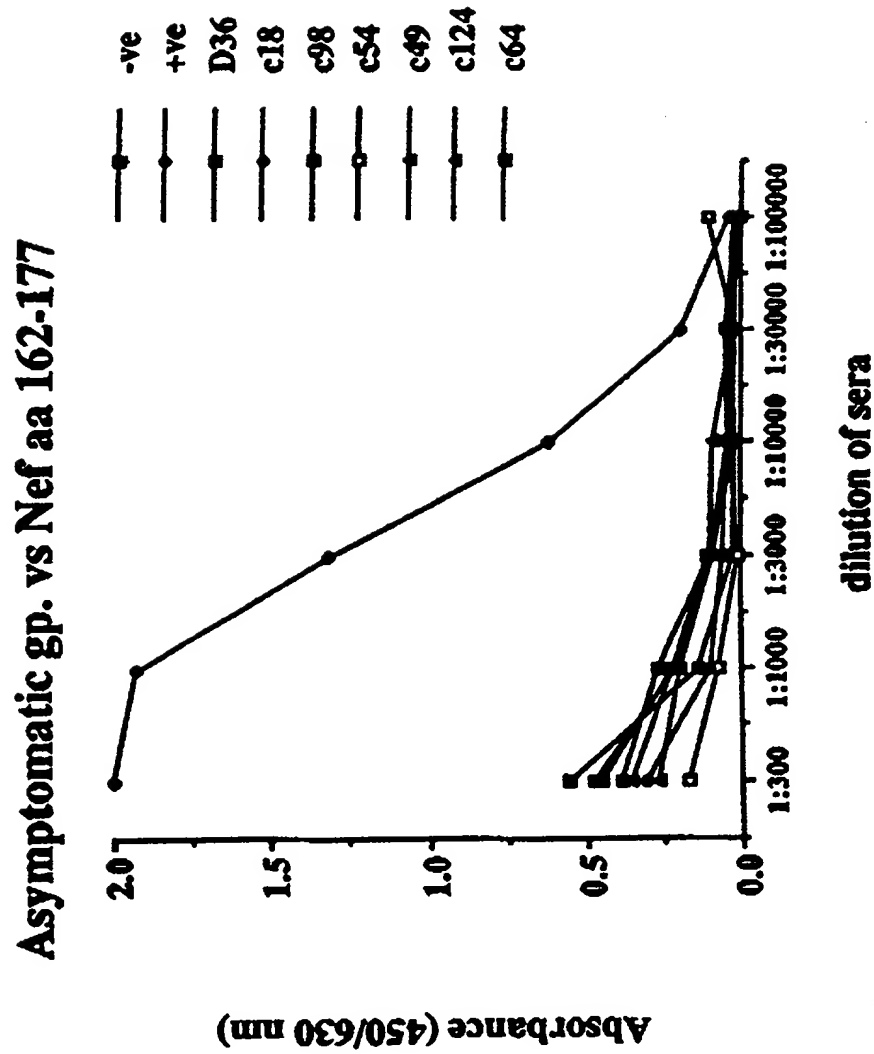


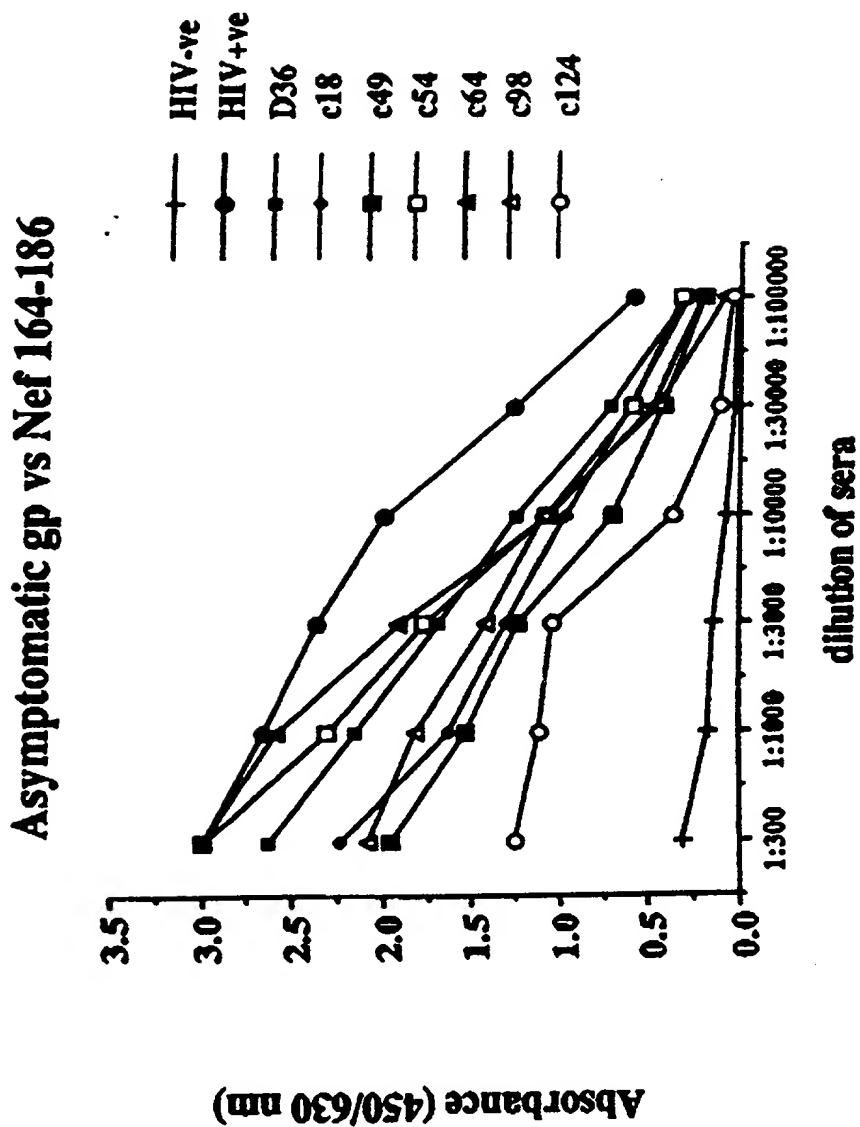
FIGURE 13C (vii)





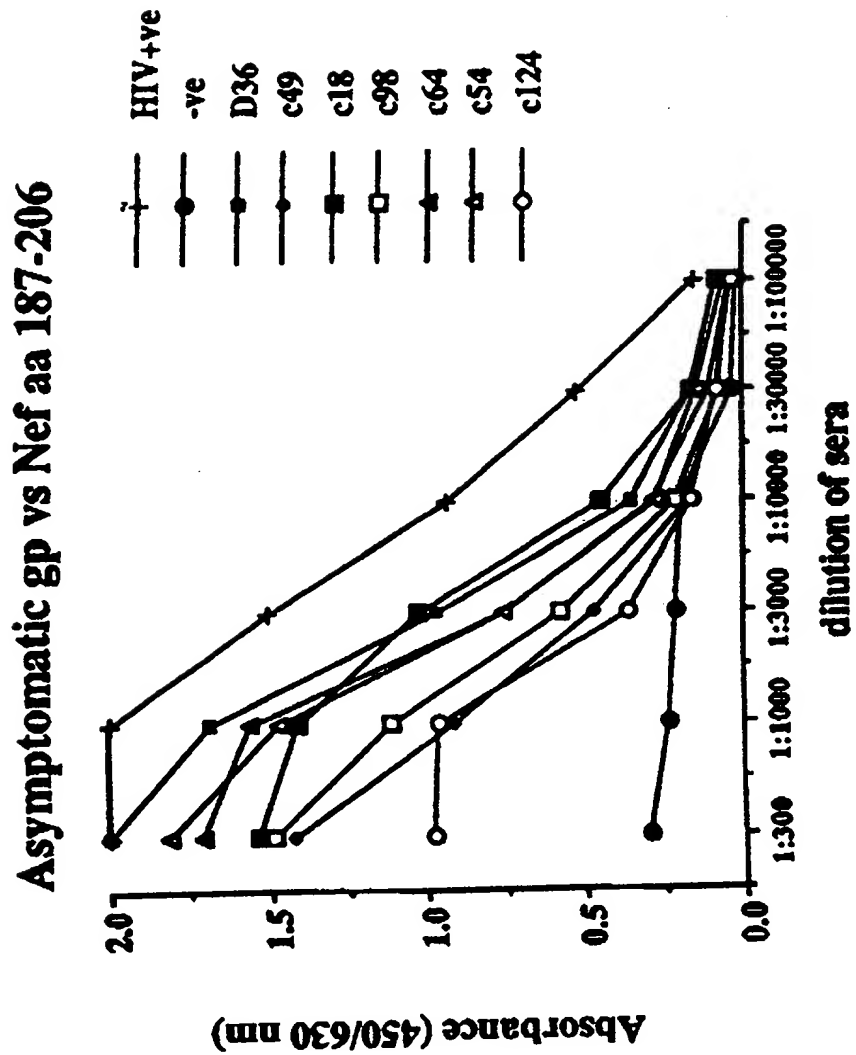
90/101

FIGURE 13C (ix)



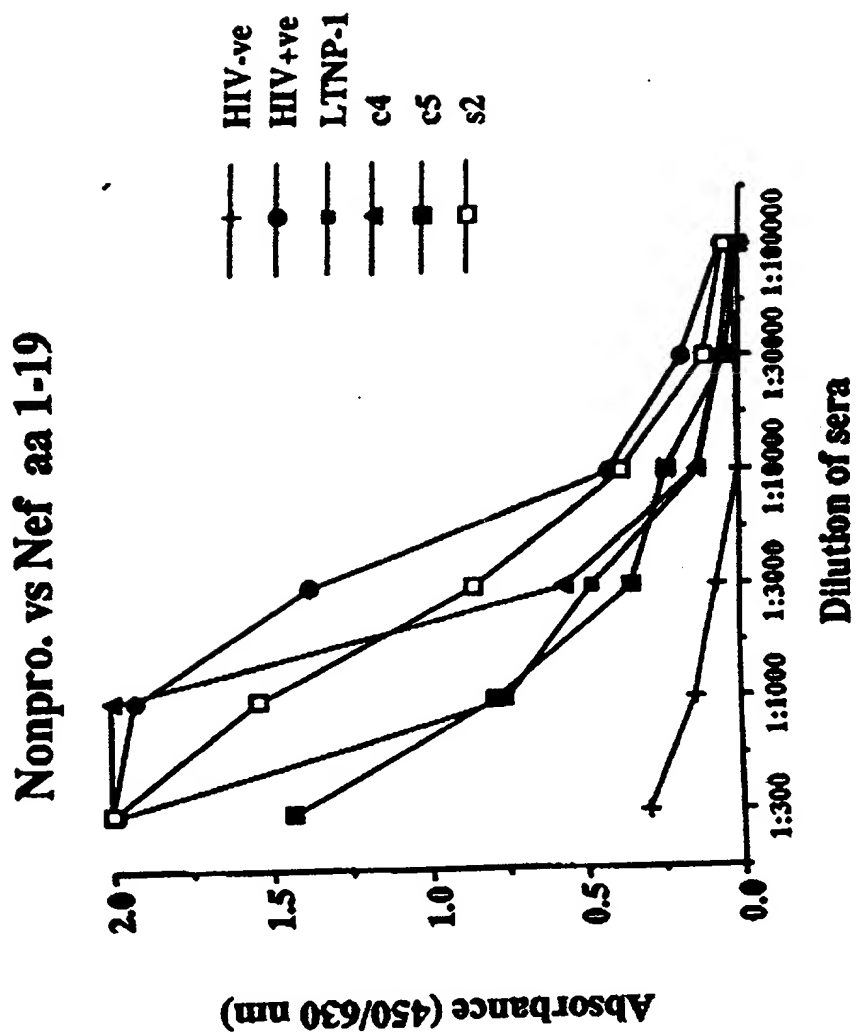
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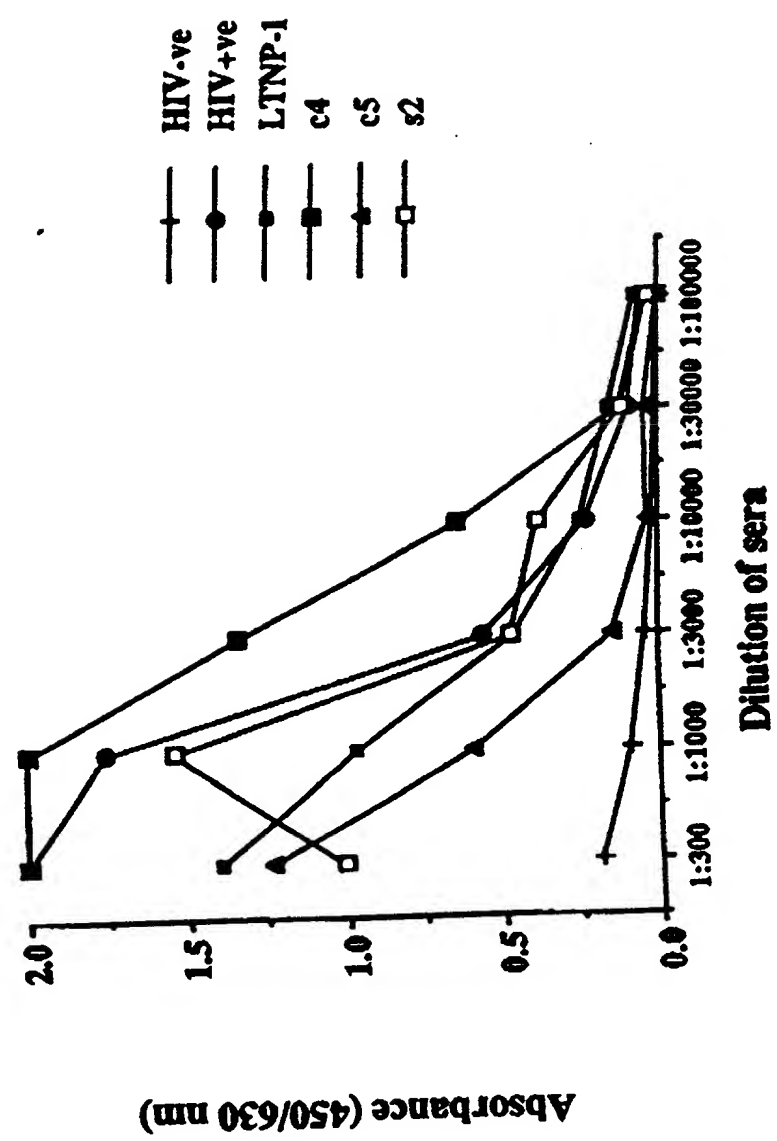
92/101

FIGURE 13D (i)



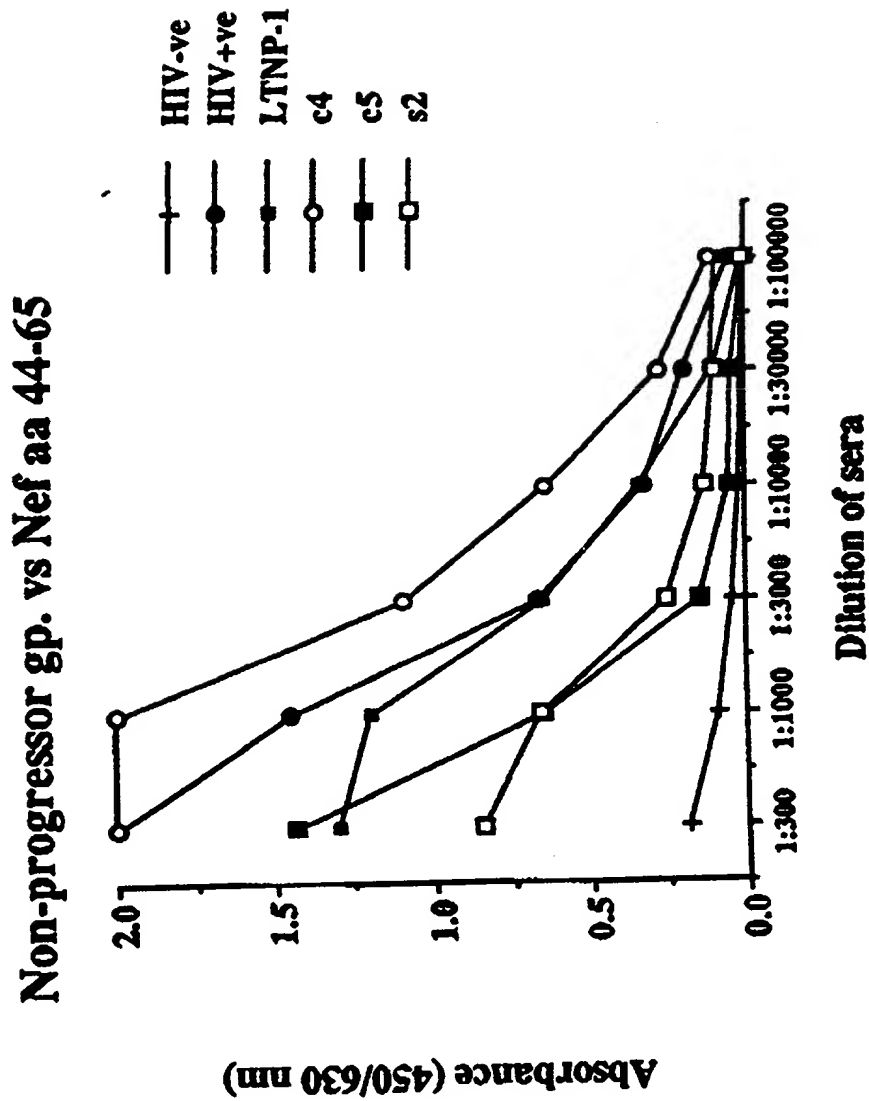
93/101
FIGURE 13D (ii)

Non-progressor. vs Nef aa 20-36



94/101

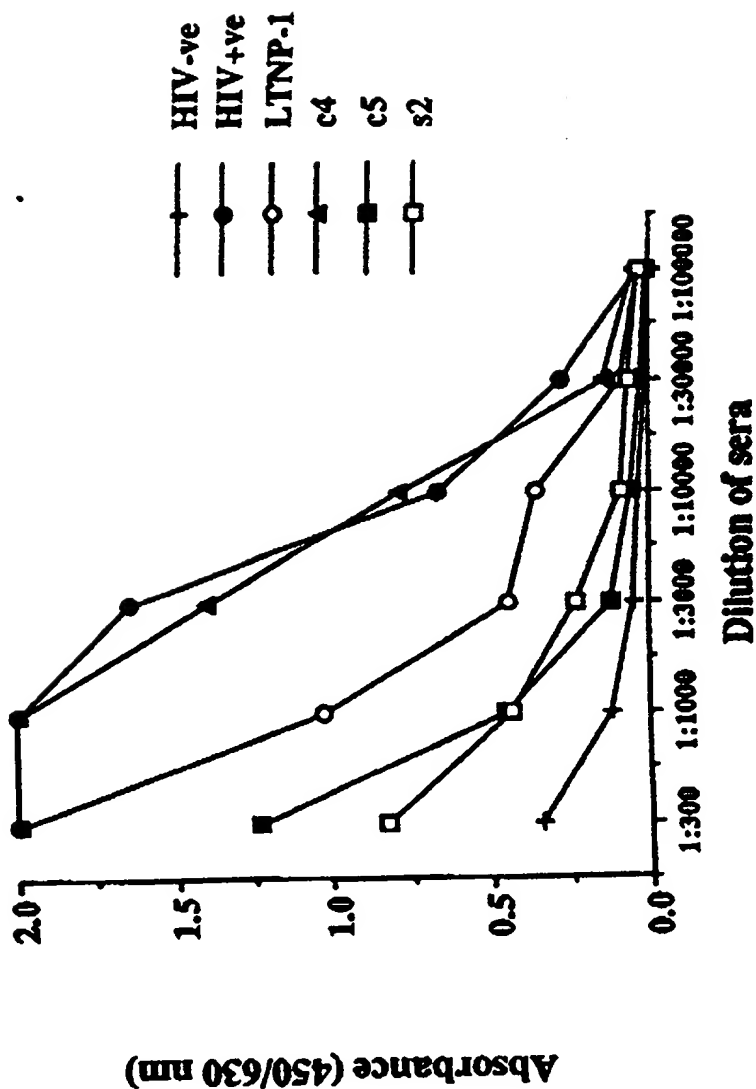
FIGURE 13D (iii)



95/101

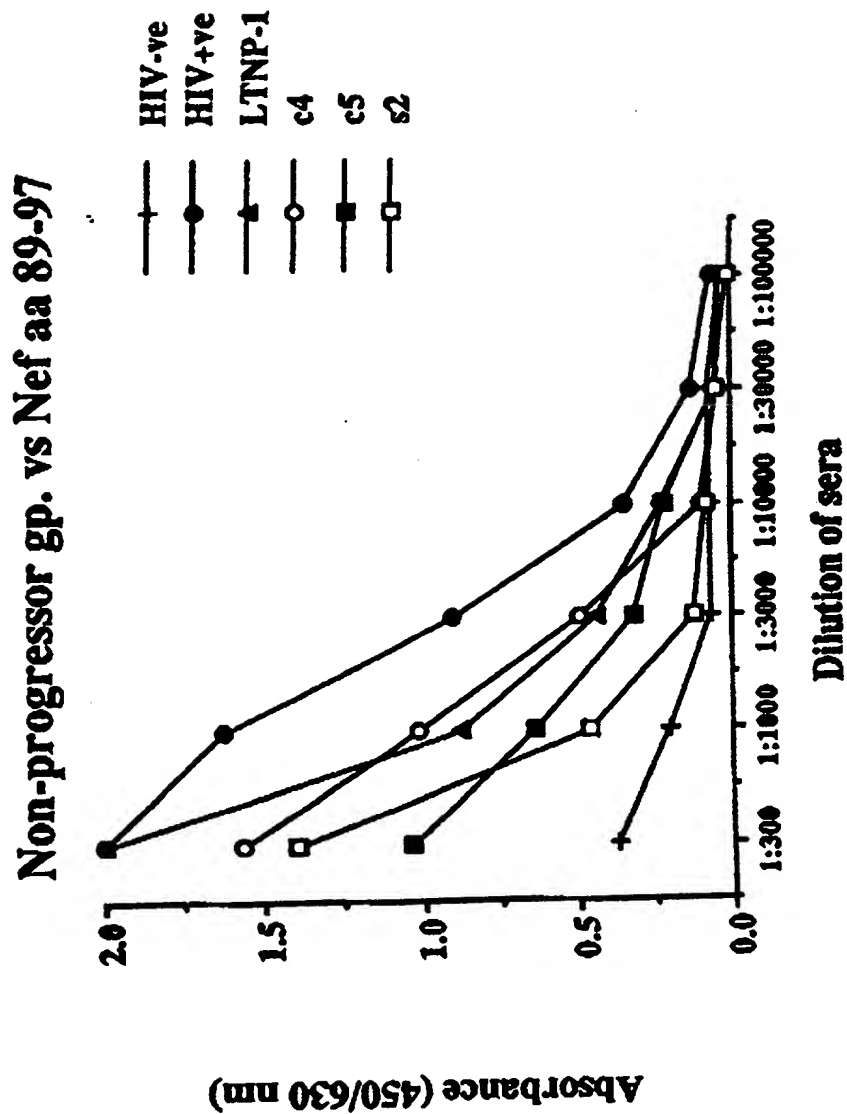
FIGURE 13D (iv)

Non-progressor gp. vs Nef aa 72-83



96/101

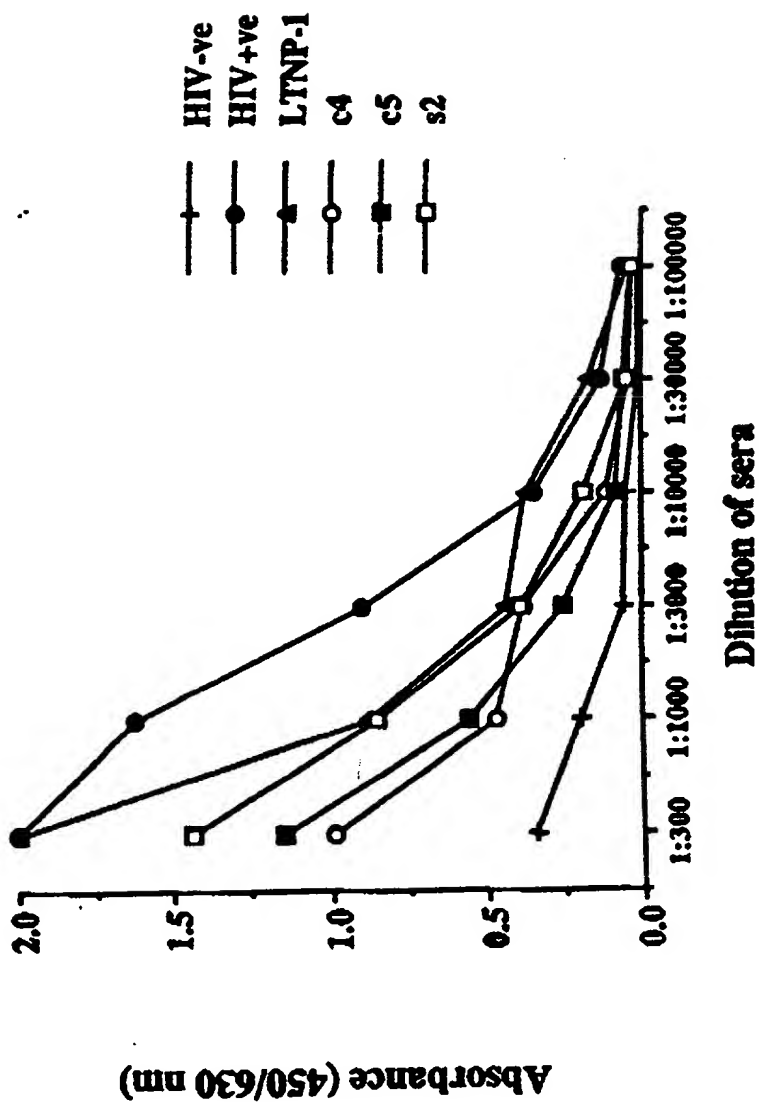
FIGURE 13D (N)



97/101

FIGURE 13D (vi)

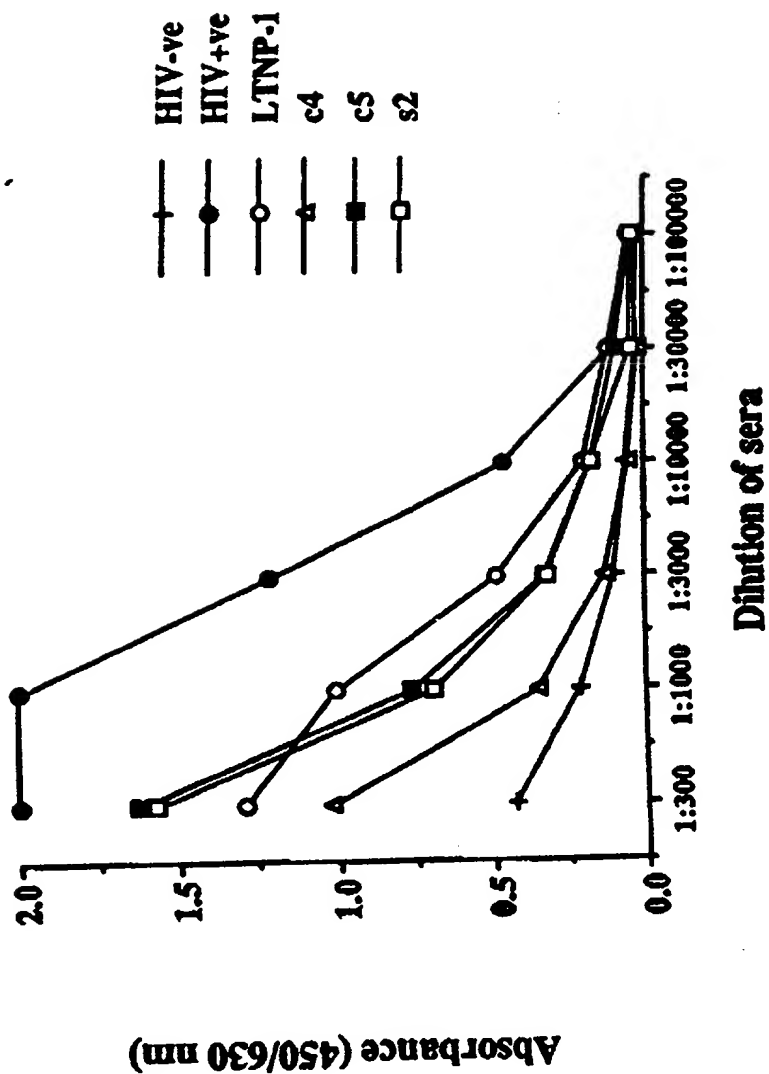
Non-progressor gp. vs Nef aa 109-114



98/101

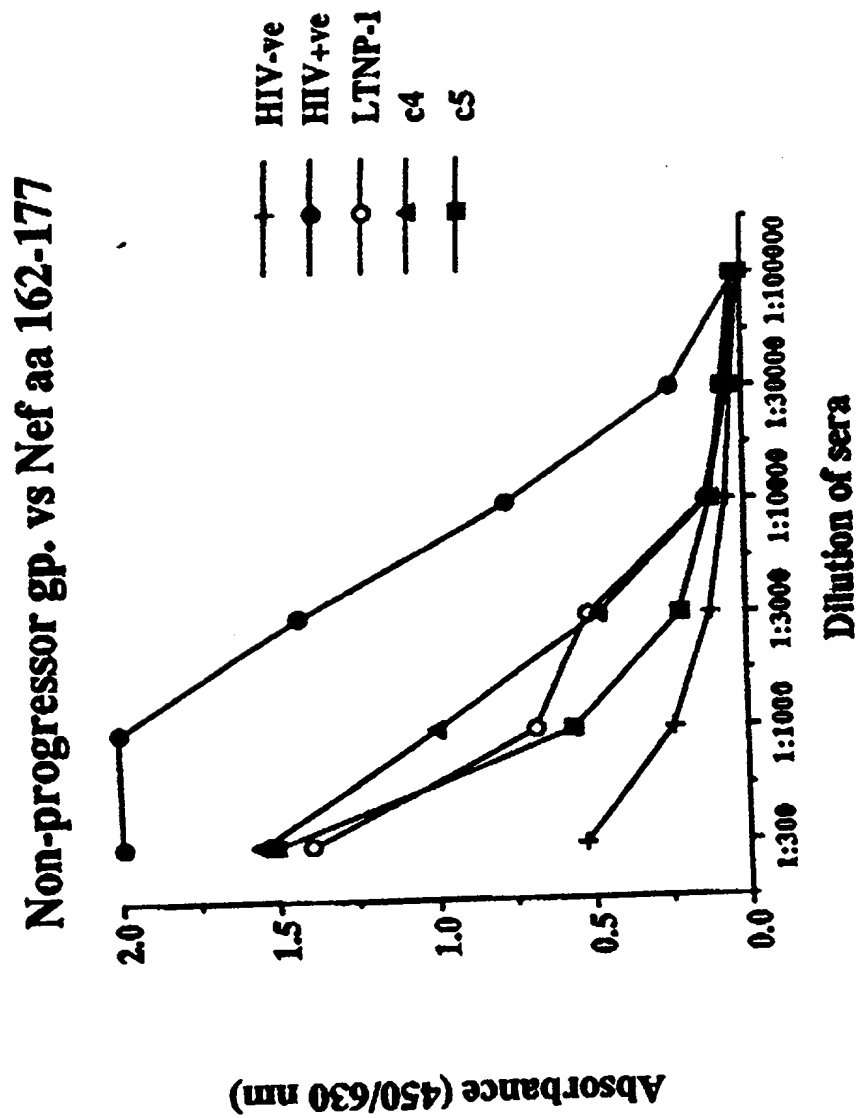
FIGURE 13D (viii)

Non-progressor gp. vs Nef aa 121-135



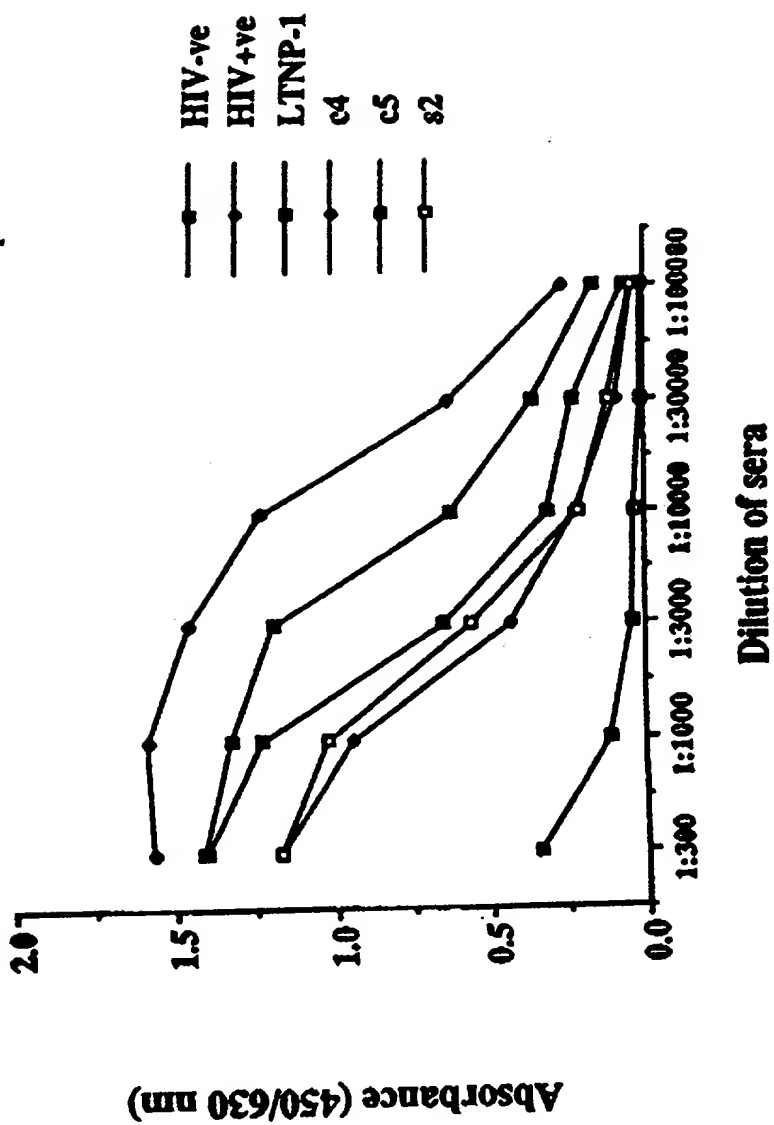
99/101

FIGURE 13D (viii)

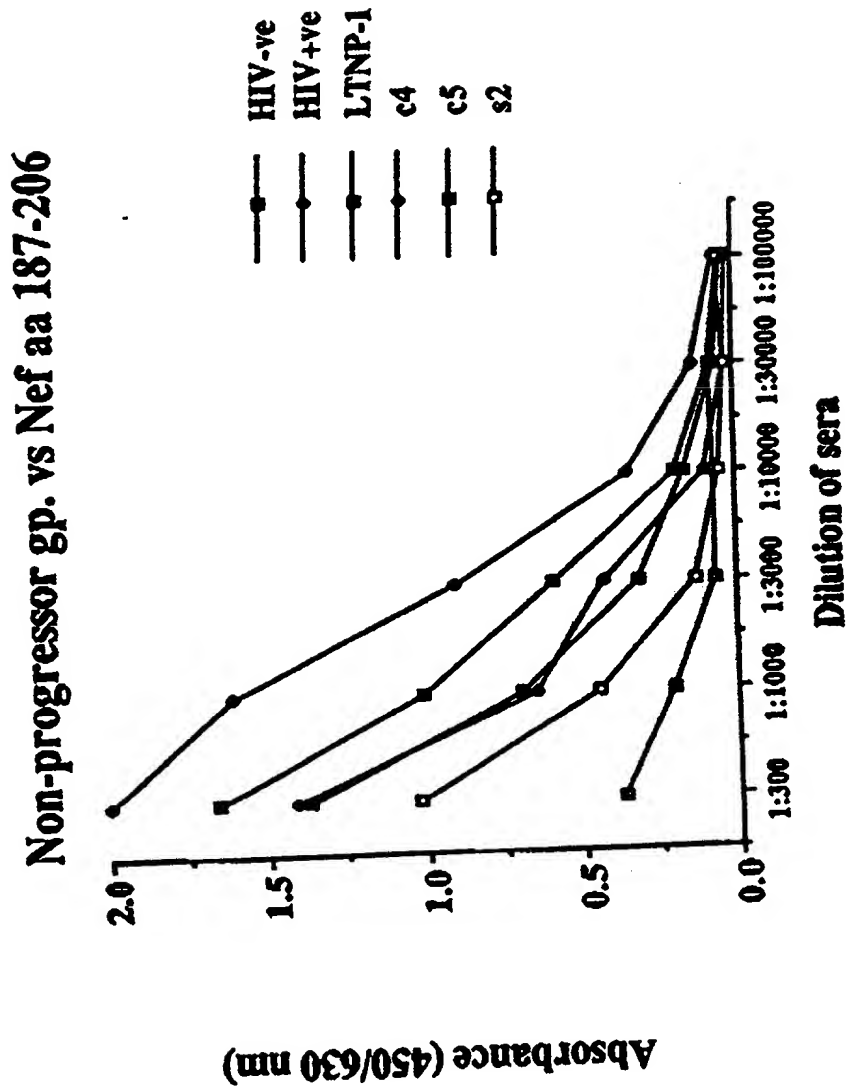


100/101
FIGURE 13D (ix)

Non-progressor gp. vs Nef aa 164-186



101/101
FIGURE 13D (x)



COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
 (Includes Reference to PCT International Applications)

 ATTORNEY'S SUBJECT NUMBER
9606Z-I

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Non-Pathogenic Strains of HIV-1

the specification of which (check only one item below):

☐ is attached hereto.

☐ was filed as United States application

Serial No. 08/477,464

on 7 June 1995

and was amended

on _____ (if applicable).

☐ was filed as PCT international application

Number _____

on _____

and was amended under PCT Article 19

on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.36(a).

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 U.S.C. 119:

COUNTRY (PCT: "INventor's Country")	APPLICATION NUMBER	DATE OF FILING (day month year)	PRIORITY CLAIM UNDER 35 USC 119
Australia	PN3021/95	17 May 1995	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO

USSN: 08/477,464

Combined Declaration For Patent Application and Power of Attorney (Continued)
 Includes Reference to PCT International Applications

 ATTORNEY'S REFERENCE NUMBER
 9606Z-I

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) or PCT international application(s) designating the United States of America that is/are listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.561(a) which occurred between the filing date of the prior application(s) and the national or PCT international filing date of this application:

PRIOR U.S. APPLICATIONS OR PCT INTERNATIONAL APPLICATIONS DESIGNATING THE U.S. FOR BENEFIT UNDER 35 U.S.C. 120:

U.S. APPLICATIONS		STATUS (Check one)		
U.S. APPLICATION NUMBER	U.S. FILING DATE	PATENTED	PENDING	ABANDONED
388,353	14 February 1995		Pending	
PCT APPLICATIONS DESIGNATING THE U.S.				
PCT APPLICATION NO.	PCT FILING DATE	U.S. SERIAL NUMBER ASSIGNED or AWAITING		

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. (List name and registration number) John F. Scully, Reg. No. 20,003; Anthony G. Scott, Reg. No. 25,439; Stephen D. Murphy, Reg. No. 27,002; Leopold Presser, Reg. No. 19,037; William C. Reed, Reg. No. 24,972; William E. McNulty, Reg. No. 22,706; Kenneth L. King, Reg. No. 20,233; Frank S. Cicciello, Reg. No. 31,346; and Paul J. Scotto, Jr., Reg. No. 20,769

Send Correspondence to:

Scully, Scott, Murphy & Presser
 400 Garden City Plaza
 Garden City, New York 11530

Direct Telephone Calls to:

William E. McNulty
 516-742-4343

2	FULL NAME OF INVENTOR	DEACON	FIRST GIVEN NAME	Nicholas	SECOND GIVEN NAME	John
	RESIDENCE & CITY	Balwyn	STATE OR FOREIGN COUNTRY	Victoria, Australia	COUNTRY OF ORIGIN	Australia
	POST OFFICE ADDRESS	51 Elliott Street	CITY	Balwyn, Victoria	STATE & POST CODE, COUNTRY	3105, Australia
2	FULL NAME OF INVENTOR	LEARMONT	FIRST GIVEN NAME	Jennifer	SECOND GIVEN NAME	Catherine
	RESIDENCE & CITY	Patongo	STATE OR FOREIGN COUNTRY	New South Wales, Australia	COUNTRY OF ORIGIN	Australia
	POST OFFICE ADDRESS	88 Patongo Street	CITY	Patongo, N.S.W.	STATE & POST CODE, COUNTRY	2256, Australia
2	FULL NAME OF INVENTOR	McPHEE	FIRST GIVEN NAME	Dale	SECOND GIVEN NAME	Alan
	RESIDENCE & CITY	Fitzroy	STATE OR FOREIGN COUNTRY	Victoria, Australia	COUNTRY OF ORIGIN	Australia
	POST OFFICE ADDRESS	14 Freeman Street	CITY	Fitzroy, Victoria	STATE & POST CODE, COUNTRY	3065, Australia

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

SIGNATURE OF INVENTOR 1	SIGNATURE OF INVENTOR 2	SIGNATURE OF INVENTOR 3
<i>[Signature]</i>	<i>[Signature]</i>	<i>[Signature]</i>
DATE	DATE	DATE
13.11.95	10.11.95	11.11.95

() Signature for fourth and subsequent joint inventors.
 Number of pages added _____

USSN: 08/477,464

Dkt: 9606Z-I

204	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
205	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
206	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
207	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
208	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
209	FULL NAME OF INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
	POST OFFICE ADDRESS	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF ORIGIN
<p>I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.</p>				
SIGNATURE OF INVENTOR 204		SIGNATURE OF INVENTOR 205		SIGNATURE OF INVENTOR 206
DATE		DATE		DATE
SIGNATURE OF INVENTOR 207		SIGNATURE OF INVENTOR 208		SIGNATURE OF INVENTOR 209
DATE		DATE		DATE

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